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OM protein - protein search, using sw model

Run on: March 7, 2003, 11:19:49 ; Search time 38 seconds
(without alignments)
1213.282 Million cell updates/sec

Title: US-09-909-775-2

Perfect score: 1879

Sequence: 1 MFLSILVALCLWLHLGVR.....SPKKNIKTRSAQKRTNPKRV 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1879	100.0	346	21 AAB00193	Breast cancer prot
2	1879	100.0	346	22 AAB76853	Human lung tumour
3	1879	100.0	346	23 ABG61803	Prostate cancer-as
4	1879	100.0	346	23 AA085508	Clone #19118 of lu
5	1879	100.0	346	23 AA014432	Human frizzled rel
6	1870	99.5	368	19 AAW73508	Human ATG-1639 pro
7	1865	99.3	346	22 AAB48183	Human FRAZZLED pol
8	1865	99.3	368	20 AAY03232	Full length sequen
9	1862	99.1	368	20 AAW86346	Human FRAZZLED pro
10	1850	98.5	347	20 AAY03231	Amino acid sequenc

11	1807	96.2	346	21 AAB23911	Bos taurus Frazzle
12	1765	93.9	372	20 AAB86347	Partial human FRAZ
13	1765	93.9	372	22 AAB48184	Partial amino acid
14	831	44.2	325	19 AAW41767	Human hsfz protein
15	831	44.2	325	19 AAW48694	Bovine growth-indu
16	831	44.2	325	20 AAY03233	Amino acid sequenc
17	830	44.2	323	19 AAW41768	Mouse hsfz protein
18	830	44.2	323	19 AAW41253	Mouse "frazzled" f
19	830	44.2	323	23 ABB57262	Mouse ischaemic co
20	828	44.1	325	19 AAW48695	Human growth-indu
21	828	44.1	325	19 AAW41254	Human "frazzled" f
22	824	43.9	325	20 AAY03229	Amino acid sequenc
23	824	43.9	325	21 AAB10281	Xenopus sp embryo
24	817.5	43.5	319	19 AAW48696	Xenopus growth-ind
25	816	43.4	318	19 AAW41251	Xenopus "frazzled"
26	812.5	43.2	171	23 ABP41377	Human ovarian anti
27	698.5	37.2	143	20 AAY48252	Human prostate can
28	621.5	33.1	261	19 AAW41766	Hamster BHKsfz pro
29	338.5	18.0	585	18 AAW31271	Human frizzled-5 p
30	319	17.0	694	18 AAW31267	Drosophila frizzle
31	318	16.9	694	22 ABB71797	Drosophila melanog
32	308	16.4	694	23 AAU74823	Human REPTR 6 prot
33	305	16.2	685	18 AAW31274	Mouse frizzled-8 p
34	300.5	16.0	647	21 AAB12117	Hydrophobic domain
35	298.5	15.9	572	18 AAW31273	Mouse frizzled-7 p
36	289	15.4	589	22 ABB71245	Drosophila melanog
37	282	15.0	581	22 AAB73308	Human frizzled fam
38	275	14.6	582	22 AAB73307	Mouse frizzled fam
39	265	14.1	540	21 AAY90903	Human frizzled-4 p
40	263.5	14.0	666	18 AAW31268	Mouse frizzled-4 p
41	262.5	14.0	338	20 AAY30157	Amino acid sequenc
42	262.5	14.0	468	22 ABB12060	Human Frizzled-3 h
43	262.5	14.0	666	20 AAY30156	Amino acid sequenc
44	255	13.6	537	18 AAW31270	Mouse frizzled-4 p
45	255	13.6	537	23 ABB57288	Mouse ischaemic co

ALIGNMENTS

RESULT 1

AAB00193
ID AAB00193 standard; Protein; 346 AA.

AC AAB00193;

DT 08-FEB-2001 (first entry)

DE Breast cancer protein BCX2.

Breast cancer; diagnosis; prognosis; detection; screening;

antibody; oestrogen receptor; anti-oestrogen; immune response;

lymph node; metastases; tumour; BCR3; BCQ8; BCQ5; BCH1; BCN1; BCN2;

BCN5; BCO2; BCX2; BCX3; BCA2; BCR2; BCJ7; BCY3; human.

OS Homo sapiens.

PN WO200055629-A2.

XX 21-SEP-2000.

PD 15-MAR-2000; 2000WO-US06952.

PR 15-MAR-1999; 99US-0268865.

PR 12-NOV-1999; 99US-0439878.

PR 12-NOV-1999; 99US-0440370.

PR 15-NOV-1999; 99US-0440493.

PR 16-NOV-1999; 99US-0440676.

PR 16-NOV-1999; 99US-0440677.

PR 29-NOV-1999; 99US-0450810.

PR 02-DEC-1999; 99US-0453137.

PR 08-MAR-2000; 2000US-0453137.

XX

Db 181 KVKPTLATYLSKNYSYVIAHAKIKAVQSGCNEVTTVDVKEIFKSSSPIRTQVPLTN 240
QY 241 SSCQPHILPHQDVLIMCYEWRSMMLLENCLVEKWRDQLSKRSIQWEERLQEQRTVQD 300
Db 241 SSCQPHILPHQDVLIMCYEWRSMMLLENCLVEKWRDQLSKRSIQWEERLQEQRTVQD 300
QY 301 KKTAGTSSNPPKPKGPPAPKPPASPKKNIKTRSAQKRTNPKRV 346
Db 301 KKTAGTSSNPPKPKGPPAPKPPASPKKNIKTRSAQKRTNPKRV 346
RESULT 3
ABG61803
ID ABG61803 standard; Protein: 346 AA.
AC ABG61803;
XX
XX
DT 15-AUG-2002 (first entry)
XX
XX Prostate cancer-associated protein #4.
XX Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
OS Mammalia.
XX
PN - W0200230268-A2.
XX
XX 18-APR-2002.
XX
XX 12-OCT-2001; 2001WO-US32045.
XX
PR 13-OCT-2000; 2000US-0687576.
PR 08-DEC-2000; 2000US-0733288.
PR 08-DEC-2000; 2000US-0733742.
PR 24-JAN-2001; 2001US-263957P.
PR 16-MAR-2001; 2001US-276791P.
PR 06-APR-2001; 2001US-276888P.
PR 24-APR-2001; 2001US-281922P.
PR 30-APR-2001; 2001US-286214P.
PR 04-MAY-2001; 2001US-288589P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
XX WPI; 2002-471335/50.
DR N-PSDB; ABK92118.
XX
XX Detecting a prostate cancer-associated transcript in a cell in a
PT patient, useful for diagnosing prostate cancer (PC) or screening
PT modulators of PC, by determining if prostate cancer-associated genes
PT are expressed in a prostate tissue -
XX
XX Claim 27; Page 304-305; 436pp; English.
XX
XX The present invention relates to methods of detecting a prostate
CC cancer-associated transcript in a cell from a patient. The method
CC comprises contacting a biological sample from the patient with
CC prostate cancer-associated polynucleotides (designated PC genes) that
CC selectively hybridise to a sequence that is at least 80% identical
CC to them. The prostate cancer-associated polynucleotide sequences
CC are differentially expressed in prostate tumour tissue or in
CC prostate cancer and are derived from the tissues of various
CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
CC The methods of the invention are useful for diagnosing and treating
CC prostate cancer in mammals. The prostate cancer-associated genes are
CC useful for diagnosing or treating prostate cancer, as well as for
CC identifying modulators of prostate cancer or agents that inhibit
CC prostate cancer. The nucleic acid sequences are particularly useful
CC in gene therapy, as a vaccine or in antisense applications.
CC ABG61800-ABG61944 represent prostate cancer-associated proteins.

XX SQ Sequence 346 AA;
Query Match 100.0%; Score 1879; DB 23; Length 346;
Best Local Similarity 100.0%; Pred. No. 4.6e-176; Mismatches 0; Indels 0; Gaps 0;
Matches 346; Conservative 0;
QY 1 MFLSILVALCLWLHLALGVRGAPCAVRIIPMCRHMPWNITRMPNHLHSHSTQENAILAEQ 60
Db 1 MFLSILVALCLWLHLALGVRGAPCAVRIIPMCRHMPWNITRMPNHLHSHSTQENAILAEQ 60
QY 61 YEELVDVNCSAVLRFFFCFCAVAPICITLFLHDPKPKSVQCRARDCEPLMKYNHNSWP 120
Db 61 YEELVDVNCSAVLRFFFCFCAVAPICITLFLHDPKPKSVQCRARDCEPLMKYNHNSWP 120
QY 121 ESLACDELPHYDRGVCISPEAIVTDLPEDVKWIDITPDMVVOERPLVDCKRLSPDRCKC 180
Db 121 ESLACDELPHYDRGVCISPEAIVTDLPEDVKWIDITPDMVVOERPLVDCKRLSPDRCKC 180
QY 181 KVKPTLATYLSKNYSYVIAHAKIKAVQSGCNEVTTVDVKEIFKSSSPIRTQVPLTN 240
Db 181 KVKPTLATYLSKNYSYVIAHAKIKAVQSGCNEVTTVDVKEIFKSSSPIRTQVPLTN 240
QY 241 SSCQPHILPHQDVLIMCYEWRSMMLLENCLVEKWRDQLSKRSIQWEERLQEQRTVQD 300
Db 241 SSCQPHILPHQDVLIMCYEWRSMMLLENCLVEKWRDQLSKRSIQWEERLQEQRTVQD 300
QY 301 KKTAGTSSNPPKPKGPPAPKPPASPKKNIKTRSAQKRTNPKRV 346
Db 301 KKTAGTSSNPPKPKGPPAPKPPASPKKNIKTRSAQKRTNPKRV 346
RESULT 4
AAU85508
ID AAU85508 standard; Protein: 346 AA.
XX
XX AAU85508;
XX
DT 21-MAY-2002 (first entry)
XX
XX Clone #19118 of lung tumour protein.
DE Lung tumour; cancer; T cell; immune response stimulator;
KW cytostatic.
XX
XX Homo sapiens.
OS
XX
XX W0200204514-A2.
PN
XX
XX 17-JAN-2002.
XX
XX 10-JUL-2001; 2001WO-US22058.
XX
XX 11-JUL-2000; 2000US-0614124.
PR 29-AUG-2000; 2000US-0651563.
PR 08-SEP-2000; 2000US-0658824.
PR 26-SEP-2000; 2000US-0671325.
PR 06-OCT-2000; 2000US-0677419.
PR 30-OCT-2000; 2000US-0702705.
PR 13-DEC-2000; 2000US-0736457.
PR 03-MAY-2001; 2001US-0849626.
XX
XX (CORI-) CORIXA CORP.
PA
XX Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
PI Warnerakis M, Carter D, Fanger GR, Vedwick TS, Bangur CS;
PI Mcnabb A, Wang A, Fanger N, Switzer A, Mcneill PD, Clapper JD;
XX WPI; 2002-164634/21.
DR N-PSDB; ABK38056.
XX
XX Novel polynucleotide encoding a lung tumour polypeptide useful for
PT stimulating and/or expanding T cells specific for a tumour protein -

XX PS Example 1: SEQ ID No 329; 223pp; English.

XX CC The invention describes an isolated polynucleotide and polypeptide
 CC useful for stimulating and/or expanding T cells specific for a tumour
 CC protein for determining the presence of a cancer in a patient. A
 CC composition containing the polynucleotide and/or polypeptide is useful
 CC for treating a lung cancer in a patient. The polypeptide is useful for
 CC removing tumour cells from a biological sample. The polynucleotide is
 CC also useful as probe or primer to detect the level of mRNA encoding a
 CC tumour protein. This is the amino acid sequence of a lung tumour
 CC associated protein, described in the method of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 346 AA;

Query Match 100.0%; Score 1879; DB 23; Length 346;
 Best Local Similarity 100.0%; Pred. No. 4.6e-176;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFLSILVALCLHLALGVGACAVRIPMCRHMPNITRMPNHLHHSTQENAILAEQ 60
 DB 1 MFLSILVALCLHLALGVGACAVRIPMCRHMPNITRMPNHLHHSTQENAILAEQ 60

QY 61 YEELVDVNCSAVLRFPPFCAMYPICITLFLHDPIKPKCKVCQARDDCEPLMKMYNHSWP 120
 DB 61 YEELVDVNCSAVLRFPPFCAMYPICITLFLHDPIKPKCKVCQARDDCEPLMKMYNHSWP 120

QY 121 ESLACDELPLYDRGVCSIPAIVTDLDPEDVKWIDITPDMVQERPLDVCCKRLSPDRCKC 180
 DB 121 ESLACDELPLYDRGVCSIPAIVTDLDPEDVKWIDITPDMVQERPLDVCCKRLSPDRCKC 180

QY 181 KVKPTLATYLSKNYSVVIHAKIKAVQSGCNEVTVDVKKEIFKSSSPTRQVPLITN 240
 DB 181 KVKPTLATYLSKNYSVVIHAKIKAVQSGCNEVTVDVKKEIFKSSSPTRQVPLITN 240

QY 241 SSCQCPHILPHQDVLIMCYEWRSMMLLENCLVEKWRDQLSKRSIQWEERLQEQRRTVQD 300
 DB 241 SSCQCPHILPHQDVLIMCYEWRSMMLLENCLVEKWRDQLSKRSIQWEERLQEQRRTVQD 300

QY 301 KKTAGTSTRSNPPKPKGPPAPKPPASPKKNIKTRSAQKRTNPKRV 346
 DB 301 KKTAGTSTRSNPPKPKGPPAPKPPASPKKNIKTRSAQKRTNPKRV 346

RESULT 5
 ID AAO14432
 AC AAO14432 standard; Protein; 346 AA.

XX AC AAO14432;
 XX DT 03-MAY-2002 (first entry)
 XX DE Human frizzled related protein 4 (FRP-4).
 XX KW Human; phosphate homeostasis modulation; frizzled related protein-4;
 KW FRP-4; phosphate transportation; serum phosphate concentration;
 KW hypophosphataemia; phosphaturia; 1,25-dihydroxy vitamin D deficiency;
 KW osteomalacia; phosphate homeostasis related disease;
 KW x-linked hypophosphataemia; rickets; oncogenic osteomalacia;
 KW rhabdomyolysis; cardiomyopathy; tumoral calcinosis; renal failure;
 KW bone mineralisation.

XX OS Homo sapiens.
 XX PN WO200205857-A2.
 XX PD 24-JAN-2002.
 XX PF 19-JUL-2001; 2001WO-US23014.

XX PR 19-JUL-2000; 2000US-219365P.
 PR 12-JAN-2001; 2001US-261438P.
 XX PA (GENZ) GENZYME CORP.
 XX PI Schlavi S, Madden SL, Manavalan P, Levine M, De Beur SJ;
 XX DR WPI; 2002-179752/23.
 DR N-PSDB; AAL41901.
 XX PT Modulating phosphate homeostasis in a subject, for alleviating the
 PT oncogenic osteomalacia-associated symptoms, comprises altering the
 PT activity of frizzled related protein-4 (FRP4) or a gene encoding FRP-4
 PT polypeptide .
 XX PS Disclosure; Fig 2; 51pp; English.

XX SQ Sequence 346 AA;
 Query Match 100.0%; Score 1879; DB 23; Length 346;
 Best Local Similarity 100.0%; Pred. No. 4.6e-176;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFLSILVALCLHLALGVGACAVRIPMCRHMPNITRMPNHLHHSTQENAILAEQ 60
 DB 1 MFLSILVALCLHLALGVGACAVRIPMCRHMPNITRMPNHLHHSTQENAILAEQ 60

QY 61 YEELVDVNCSAVLRFPPFCAMYPICITLFLHDPIKPKCKVCQARDDCEPLMKMYNHSWP 120
 DB 61 YEELVDVNCSAVLRFPPFCAMYPICITLFLHDPIKPKCKVCQARDDCEPLMKMYNHSWP 120

QY 121 ESLACDELPLYDRGVCSIPAIVTDLDPEDVKWIDITPDMVQERPLDVCCKRLSPDRCKC 180
 DB 121 ESLACDELPLYDRGVCSIPAIVTDLDPEDVKWIDITPDMVQERPLDVCCKRLSPDRCKC 180

QY 181 KVKPTLATYLSKNYSVVIHAKIKAVQSGCNEVTVDVKKEIFKSSSPTRQVPLITN 240
 DB 181 KVKPTLATYLSKNYSVVIHAKIKAVQSGCNEVTVDVKKEIFKSSSPTRQVPLITN 240

QY 241 SSCQCPHILPHQDVLIMCYEWRSMMLLENCLVEKWRDQLSKRSIQWEERLQEQRRTVQD 300
 DB 241 SSCQCPHILPHQDVLIMCYEWRSMMLLENCLVEKWRDQLSKRSIQWEERLQEQRRTVQD 300

QY 301 KKTAGTSTRSNPPKPKGPPAPKPPASPKKNIKTRSAQKRTNPKRV 346
 DB 301 KKTAGTSTRSNPPKPKGPPAPKPPASPKKNIKTRSAQKRTNPKRV 346

RESULT 6
 ID AAW73508
 AC AAW73508 standard; Protein; 368 AA.
 XX

CC standard ligand/receptor binding techniques. The present sequence
XX represents the human FRAZZLED polypeptide.
SQ Sequence 346 AA;

Query Match 99.3%; Score 1865; DB 22; Length 346;
Best Local Similarity 99.4%; Pred. No. 1.1e-174;
Matches 344; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFLSILVALCLWLHLALGVGAPCEAVRIPMCRHMPWNITRMPNHLHSHSTQENAILAIEQ 60
|||||
Db 1 MFLSILVALCLWLHLALGVGAPCEAVRIPMCRHMPWNITRMPNHLHSHSTQENAILAIEQ 60
|||||

QY 61 YEELVDVNCSAVLRFFFFCAMYPACTLEFLHDPKPKSVQCRARDCEPLMKMYNHSWP 120
|||||
Db 61 YEELVDVNCSAVLRFFFFCAMYPACTLEFLHDPKPKSVQCRARDCEPLMKMYNHSWP 120
|||||

QY 121 ESLACDELPLYDRGVCIISPAIVTDLPEYKWDITPDMMVQERPLDVCCKRLSPDRCKC 180
|||||
Db 121 ESLACDELPLYDRGVCIISPAIVTDLPEYKWDITPDMMVQERPLDVCCKRLSPDRCKC 180
|||||

QY 181 KVKPTLATYLSKNYSYVIAKIKAVQSGCNEVTVVDVKEIFKSSSPIPTQVPLITN 240
|||||
Db 181 KVKPTLATYLSKNYSYVIAKIKAVQSGCNEVTVVDVKEIFKSSSPIPTQVPLITN 240
|||||

QY 241 SSCQCPHILPHQDVLIMCYEWRSRMMLLENCLVEKWRDQLSKRSIQWEERLQQRRTVQD 300
|||||
Db 241 SSCQCPHILPHQDVLIMCYEWRSRMMLLENCLVEKWRDQLSKRSIQWEERLQQRRTVQD 300
|||||

QY 301 KKKTAGTSSRNPCKPKGPPAPKSPKKNIKTRSAQKRTNPKRV 346
|||||
Db 301 KKKTAGTSSRNPCKPKGPPAPKSPKKNIKTRSAQKRTNPKRV 346
|||||

RESULT 8
AAV03232
ID AAY03232 standard; Protein: 368 AA.

XX AC AAY03232;
DT 16-AUG-1999 (first entry)
XX

DE -Full length sequence of the human frezzled-like protein.
XX
KW Human frezzled-like protein; HFLP; frizzled protein family;
KW differentiation-related disorder; agonist; antagonist; antibody;
KW haematopoiesis; wound healing; cancer; inflammatory disorder;
KW autoimmune disease; allergic reaction.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..43
FT Protein /note= "signal peptide"
FT Protein 44..368
FT Domain /note= "mature protein"
FT FT 47..166
FT /note= "frizzled domain"
XX
PN WO9909152-A1.
XX
PD 25-FEB-1999.
XX
PF 11-AUG-1998; 98WO-US16701.
XX
PR 10-APR-1998; 98US-0081438.
PR 12-AUG-1997; 97US-0055715.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Olsen HS, Ruben SM;
XX
DR WPI; 1999-190159/16.

DR N-PSDB; AAX28656.
XX New isolated human frezzled-like protein - used to develop products
PT for treating e.g. cancers, inflammatory and autoimmune diseases,
PT infectious diseases and allergic reactions
XX
PS Claim 1; Fig 2A-2B; 152pp; English.
XX
CC This is the amino acid sequence of the full length human
CC frezzled-like protein (HFLP), used in the method of the
CC invention. It is a member of the frizzled protein family. It is
CC used in the detection and treatment of differentiation-related
CC disorders. In conditions where HFLP is under-expressed, its agonist
CC is involved in the treatment. Antagonist and antibodies of HFLP are
CC used in the treatment of disorder where HFLP is over-expressed, e.g.
CC the regulation of haematopoiesis, and wound healing. HFLP products
CC are used to develop products for treating e.g. cancers, inflammatory
CC and autoimmune diseases, infectious diseases and allergic
CC reactions.
XX
SQ Sequence 368 AA;

Query Match 99.3%; Score 1865; DB 20; Length 368;
Best Local Similarity 99.4%; Pred. No. 1.2e-174;
Matches 344; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFLSILVALCLWLHLALGVGAPCEAVRIPMCRHMPWNITRMPNHLHSHSTQENAILAIEQ 60
|||||
Db 23 MFLSILVALCLWLHLALGVGAPCEAVRIPMCRHMPWNITRMPNHLHSHSTQENAILAIEQ 82
|||||

QY 61 YEELVDVNCSAVLRFFFFCAMYPACTLEFLHDPKPKSVQCRARDCEPLMKMYNHSWP 120
|||||
Db 83 YEELVDVNCSAVLRFFFFCAMYPACTLEFLHDPKPKSVQCRARDCEPLMKMYNHSWP 142
|||||

QY 121 ESLACDELPLYDRGVCIISPAIVTDLPEYKWDITPDMMVQERPLDVCCKRLSPDRCKC 180
|||||
Db 143 ESLACDELPLYDRGVCIISPAIVTDLPEYKWDITPDMMVQERPLDVCCKRLSPDRCKC 202
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QY 181 KVKPTLATYLSKNYSYVIAKIKAVQSGCNEVTVVDVKEIFKSSSPIPTQVPLITN 240
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Db 203 KVKPTLATYLSKNYSYVIAKIKAVQSGCNEVTVVDVKEIFKSSSPIPTQVPLITN 262
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QY 241 SSCQCPHILPHQDVLIMCYEWRSRMMLLENCLVEKWRDQLSKRSIQWEERLQQRRTVQD 300
|||||
Db 263 SSCQCPHILPHQDVLIMCYEWRSRMMLLENCLVEKWRDQLSKRSIQWEERLQQRRTVQD 322
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QY 301 KKKTAGTSSRNPCKPKGPPAPKSPKKNIKTRSAQKRTNPKRV 346
|||||
Db 323 KKKTAGTSSRNPCKPKGPPAPKSPKKNIKTRSAQKRTNPKRV 368
|||||

RESULT 9
AAW86346
ID AAW86346 standard; Protein: 368 AA.

XX AC AAW86346;
DT 15-MAR-1999 (first entry)
XX
XX Human FRAZZLED protein.
XX
KW Human; FRAZZLED protein; FRZB; chronic inflammation; acute inflammation;
KW arthritis; osteoarthritis; septicaemia; autoimmune disease; cancer;
KW transplant rejection; graft versus host disease; infection; stroke;
KW ischaemia; acute respiratory disease syndrome; renal disorder;
KW restenosis; brain injury; AIDS; cancer.
XX
OS Homo sapiens.
XX
PN EP887406-A2.
XX
XX 30-DEC-1998.
XX

```
PF 23-APR-1998; 98EP-0303163..
XX
XX 26-NOV-1997; 97US-0978981.
PR 22-MAY-1997; 97US-0047408.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX James I, Kumar S, Lark M;
PI
XX WPI: 1999-047873/05.
DR N-PSDB; AAV80657.
XX
XX New FRZB -related (FRAZZLED) polypeptide and polynucleotide - useful
PT as diagnostic reagents and for prevention and treatment of cancer,
PT Alzheimer's disease and AIDS
XX
XX Claim 11; Page 7-8; 25pp; English.
XX
XX The present sequence represents human FRAZZLED protein from the FRZB
CC family. The FRZB family controls signalling and developmental
CC patterning. FRAZZLED proteins and polynucleotides are useful for
CC diagnosing diseases related to over or underexpression of FRAZZLED
CC protein by identifying mutations in the FRAZZLED gene, or determining
CC FRAZZLED protein expression levels. FRAZZLED proteins can be used to
CC screen for agonists and antagonists which bind the FRAZZLED protein
CC by observing the binding, or stimulation or inhibition of FRAZZLED
CC activity. These can be used in treatment to activate (agonist) or
CC inhibit (antagonist) FRAZZLED activity, in addition to direct
CC administration of antisense sequences to prevent expression, or FRAZZLED
CC polynucleotides to treat conditions associated with a lack of FRAZZLED
CC protein. Gene therapy may also be used to affect endogenous FRAZZLED
CC protein production. FRAZZLED antibodies are useful for inducing an
CC immune response to immunise and prevent diseases, and for isolating
CC FRAZZLED clones or purifying the protein by affinity chromatography.
CC FRAZZLED proteins can be administered directly or as a vaccine to
CC inoculate against diseases. Diseases diagnosed, prevented or treated
CC include: chronic and acute inflammation, arthritis, osteoarthritis,
CC septicemia, autoimmune diseases, transplant rejection, graft versus
CC host disease, infection, stroke, ischaemia, acute respiratory disease
CC syndrome, renal disorders, restenosis, brain injury, AIDS and cancer.
XX
XX Sequence 368 AA;
SQ
Query Match 99.1%; Score 1862; DB 20; Length 368;
Best Local Similarity 99.1%; Pred. No. 2.3e-174;
Matches 343; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MFLSILVALCLWLHLALGVGAPCEAVRIPMCRHMPWNTTRPNHLHSHSTQENAILAIEQ 60
DB 23 MFLSILVALCLWLHLALGVGAPCEAVRIPMCRHMPWNTTRPNHLHSHSTQENAILAIEQ 82
QY 61 YEELVDVNCSAVLRFFFCAMYPICITLFLHPDIKPKCSVCORARDCEPLMKMNHNSWP 120
DB 83 YEELVDVNCSAVLRFFFCAMYPICITLFLHPDIKPKCSVCORARDCEPLMKMNHNSWP 142
QY 121 ESLACDELVPYDRGVCISPEAIVTDLPEVKWIDITPDMVMQERPLDVCRLSPDRCK 180
DB 143 ESLACDELVPYDRGVCISPEAIVTDLPEVKWIDITPDMVMQERPLDVCRLSPDRCK 202
QY 181 KVKKPTLATYLSKNYSYVTHAKIKAVQSGCNEVTVVDVKEIFKSSSPIPTQVPLITN 240
DB 203 KVKKPTLATYLSKNYSYVTHAKIKAVQSGCNEVTVVDVKEIFKSSSPIPTQVPLITN 262
QY 241 SSCQCPHILPHODVLIMCYEWSRMMLLENCLVEKWRDLSKRSIQWEERLOPQRTVOD 300
DB 263 SSCQCPHILPHODVLIMCYEWSRMMLLENCLVEKWRDLSKRSIQWEERLOPQRTVOD 322
QY 301 KKKTAGRTSRSPKPKGPPAPKSPASPKKNIKTRSAQRTPKRV 346
DB 323 KKKTAGRTSRSPKPKGTPAPKSPASPKKNIKTRSAQRTPKRV 368
RESULT 10
```

```
AAAY03231
ID AAY03231 standard; Protein; 347 AA.
XX
AC AAY03231;
XX
XX 16-AUG-1999 (first entry)
XX
XX Amino acid sequence of the human frezzled-like protein.
XX
XX Human frezzled-like protein; HFLP; frizzled protein family;
KW differentiation-related disorder; agonist; antagonist; antibody;
KW haematopoiesis; wound healing; cancer; inflammatory disorder;
KW autoimmune disease; allergic reaction.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..19
FT /note= "signal peptide"
FT Protein 20..347
FT /note= "mature protein"
FT Domain 25..145
FT /note= "frizzled domain"
XX
XX WO9909152-A1.
XX
XX 25-FEB-1999.
XX
XX 11-AUG-1998; 98WO-US16701.
XX
XX 10-APR-1998; 98US-0081438.
PR 12-AUG-1997; 97US-0055715.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Olsen HS, Ruben SM;
PI
XX WPI: 1999-190159/16.
DR N-PSDB; AAX28655.
XX
XX New isolated human frezzled-like protein - used to develop products
PT for treating e.g. cancers, inflammatory and autoimmune diseases,
PT infectious diseases and allergic reactions
XX
XX Claim 1; Fig 1A-1B; 152pp; English.
XX
XX This is the amino acid sequence of the human frezzled-like
CC protein (HFLP), used in the method of the invention. It is a
CC member of the frizzled protein family. It is used in the detection
CC and treatment of differentiation-related disorders. In conditions
CC where HFLP is under-expressed, its agonist is involved in the
CC treatment. Antagonist and antibodies of HFLP are used in the
CC treatment of disorder where HFLP is over-expressed, e.g. the
CC regulation of haematopoiesis, and wound healing. HFLP products are
CC used to develop products for treating e.g. cancers, inflammatory
CC and autoimmune diseases, infectious diseases and allergic
CC reactions.
XX
XX Sequence 347 AA;
SQ
Query Match 98.5%; Score 1850; DB 20; Length 347;
Best Local Similarity 99.4%; Pred. No. 3.3e-173;
Matches 341; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 SILVALCLWLHLALGVGAPCEAVRIPMCRHMPWNTTRPNHLHSHSTQENAILAIEQYEE 63
DB 5 SILVALCLWLHLALGVGAPCEAVRIPMCRHMPWNTTRPNHLHSHSTQENAILAIEQYEE 64
QY 64 LYDVNCSAVLRFFFCAMYPICITLFLHPDIKPKCSVCORARDCEPLMKMNHNSWPESL 123
DB 65 LYDVNCSAVLRFFFCAMYPICITLFLHPDIKPKCSVCORARDCEPLMKMNHNSWPESL 124
QY 124 ACDELVPYDRGVCISPEAIVTDLPEVKWIDITPDMVMQERPLDVCRLSPDRCKKV 183
```

DB 125 ACDELPLYDRGVCSPEAIVTDLPEYDKWIDITPDMMVQERPLDVCKRLSPDRCKKV 184
 QY 184 KPTLATYLSKNYSYVTHAKIKAVORSGCNEVTVVDVKKEIFKSSSIPRTQVPLITNSSC 243
 DB 185 KPTLATYLSKNYSYVTHAKIKAVORSGCNEVTVVDVKKEIFKSSSIPRTQVPLITNSSC 244
 QY 244 QCPHILPHODVLIMCYEWSRMMLLENCLVEKWRDQLSKRSIQWEERLQQRRTVQDKK 303
 DB 245 QCPHILPHODVLIMCYEWSRMMLLENCLVEKWRDQLSKRSIQWEERLQQRRTVQDKK 304
 QY 304 TAGRTSRNPPKPKGPPAPKPKPKNIKTRSAQRTNPKRV 346
 DB 305 TAGRTSRNPPKPKGTPAPKPKPKNIKTRSAQRTNPKRV 347

RESULT 11

AAB23911
ID AAB23911 standard; Protein; 346 AA.

XX AAB23911;

XX 17-JAN-2001 (first entry)

DE Bos taurus Frazzled protein SEQ ID NO:2.

KW Bovine; Bos taurus; frazzled protein; FRZB family; cytostatic; antiHIV;
 KW human immunodeficiency virus; nontropic; vasotropic; neuroprotective;
 KW antiinflammatory; antiarthritic; antiarthritis; immunosuppressive;
 KW cerebroprotective; antiarteriosclerotic; osteopathic; ophthalmological;
 KW antipsoriatic; cartilage; bone morphogenesis; regulator; inflammation;
 KW arthritis; rheumatoid arthritis; osteoarthritis; septicaemia; stroke;
 KW autoimmune disease; transplant rejection; graft versus host disease;
 KW infection; ischaemia; renal disorder; restenosis; brain injury; AIDS;
 KW bone disease; osteoporosis; cancer; lymphoproliferative disorder;
 KW atherosclerosis; Alzheimer's disease; retinitis pigmentosa;
 KW macular degeneration; degenerative eye disease.

XX Bos taurus.

XX WO200055202-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06820.

XX 18-MAR-1999; 99US-0125038.

XX 03-MAR-2000; 2000US-0519397.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX James IE, Lark MW, Testa TT;

XX WPI; 2000-638181/61.

XX N-PSDB; AAA99046.

XX Novel Bos taurus Frazzled polypeptides and nucleotides encoding them,

XX useful for treating inflammation, arthritis, acquired immunodeficiency

XX syndrome (AIDS) and Alzheimer's diseases -

XX Claim 2; Page 27; 29pp; English.

XX The present sequence represents bovine (Bos taurus) Frazzled protein
 CC which is a member of the FRZB family. The frazzled protein can have
 CC cytostatic, antiHIV (human immunodeficiency virus), nontropic,
 CC vasotropic, neuroprotective, antiinflammatory, antiarthritic,
 CC antiarthritis, immunosuppressive, cerebroprotective, osteopathic,
 CC antiarteriosclerotic, ophthalmological and antipsoriatic activities,
 CC and is a regulator of cartilage and bone morphogenesis. The frazzled
 CC polynucleotide and protein are useful for treating and preventing
 CC chronic and acute inflammation, arthritis, rheumatoid arthritis,
 CC osteoarthritis, septicaemia, autoimmune diseases (e.g. inflammatory

CC bowel disease, psoriasis), transplant rejection, graft versus host
 CC disease, infection, stroke, ischaemia, acute respiratory disease
 CC syndrome, renal disorder, restenosis, brain injury, AIDS, metabolic and
 CC other bone diseases (e.g. osteoporosis), cancer (e.g. lymphoproliferative
 CC disorders), atherosclerosis, Alzheimer's disease, retinitis pigmentosa,
 CC macular degeneration and other degenerative eye diseases. The protein
 CC is also useful to establish assays to predict oral absorption and
 CC pharmacokinetics in man and thus enhance compound and formulation design,
 CC and in screening assays. The polynucleotide is useful for recombinant
 CC production of the frazzled protein.

XX Sequence 346 AA;

SQ Query Match 96.2%; Score 1807; DB 21; Length 346;
 Best Local Similarity 95.9%; Pred. No. 5.5e-169;
 Matches 331; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 MFLSILVALCLWLHLALGVGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60
 DB 1 MLLSILTALCLWLRLALGVGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60

QY 61 YEELVDVNCSAVLRFPPFCAMYPACTLEFLHDPKPKSVQORARDDCEPLMKMYNHSWP 120
 DB 61 YEELVDVNCSAVLRFPPFCAMYPACTLEFLHDPKPKSVQORARDDCEPLMKMYNHSWP 120

QY 121 ESLACDELPLYDRGVCSPEAIVTDLPEYDKWIDITPDMMVQERPLDVCKRLSPDRCKC 180
 DB 121 ESLACDELPLYDRGVCSPEAIVTDLPEYDKWIDITPDMMVQERPLDVCKRLSPDRCKC 180

QY 181 KVKVPTLATYLSKNYSYVTHAKIKAVORSGCNEVTVVDVKKEIFKSSSIPRTQVPLITN 240
 DB 181 KVKVPTLATYLSKNYSYVTHAKIKAVORSGCNEVTVVDVKKEIFKSSSIPRTQVPLITN 240

QY 241 SSCQCCHILPHODVLIMCYEWSRMMLLENCLVEKWRDQLSKRSIQWEERLQQRRTVQD 300
 DB 241 SSCQCCHILPHODVLIMCYEWSRMMLLENCLVEKWRDQLSKRSIQWEERLQQRRTVQD 300

QY 301 KKTAGRTSRNPPKPKGPPAPKPKPKNIKTRSAQRTNPKR 345
 DB 301 KKTAGRTSRNPPKPKGPPAPKPKPKNIKTRSAQRTNPKR 345

RESULT 12
 AAW86347

ID AAW86347 standard; Protein; 372 AA.

XX AAW86347;

XX 15-MAR-1999 (first entry)

DE Partial human FRAZZLED protein.

XX Human; FRAZZLED protein; FRZB; chronic inflammation; acute inflammation;
 KW arthritis; osteoarthritis; septicemia; autoimmune disease; cancer;
 KW transplant rejection; graft versus host disease; infection; stroke;
 KW ischaemia; acute respiratory disease syndrome; renal disorder;
 KW restenosis; brain injury; AIDS; cancer.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 19 /label= unknown

XX /note= "encoded by GAN"

XX EP887406-A2.

XX 30-DEC-1998.

XX 23-APR-1998; 98EP-0303163.

XX 26-NOV-1997; 97US-0978981.

XX 22-MAY-1997; 97US-0047408.

QY 120 PESLACDELPPVDRGVCISPEAIVTDLPEVKWIDITPDMVQERPLDVCKRLSPDRCK 179
 Db 143 PESLACDELPPVDRGVCISPEAIVTDLPEVKWIDITPDMVQERPLDVCKRLSPDRCK 202
 QY 180 CKVKPTLATYLSKNYSYVIHAKIKAVQSGGNEVTVVDVKEIFKSSSPIRTOVPLIT 239
 Db 203 CKVKPTLATYLSKNYSYVIHAKIKAVQSGGNEVTVVDVKEIFKSSSPIRTOVPLIT 262
 QY 240 NSSCQCQPHILPHQDVLIMCYEWRSMMLLENCLVEKWRDQLSKRSQWEERLQEQRTVQ 299
 Db 263 NSSCQCQPHILPHQDVLIMCYEWRSMMLLENCLVEKWRDQLSKRSQWEERLQEQRTVQ 322
 QY 300 DKKKTAGTSSRNPSPKPKPAPKSPKKNIKTR---SAQRTNPKRV 346
 Db 323 DKKKTAGTSSRNPSPKPKPAPKSPKKNIKTRGRTPRKRTPNPKRV 372

RESULT 14
 AAW41767
 ID AAW41767 standard; Protein; 325 AA.
 AC AAW41767;
 XX
 DT 28-SEP-1998 (first entry)
 XX
 DE Human hsfz protein.
 XX
 KW Human; nerve cell growth factor; hsfz protein; neuronal cell;
 KW proliferation; differentiation factor.
 XX
 OS Homo sapiens.
 XX
 PN DE19702835-A1.
 XX
 PD 22-JAN-1998.
 XX
 PF 27-JAN-1997; 97DE-1002835.
 XX
 PR 09-JUL-1996; 96DE-1027631.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Deutsch U; Drexler JCA, Lottspeich F, Mayr T, Risau W;
 PI Rohrer H;
 XX
 DR WPI: 1998-088096/09.
 DR N-PSDB; AAV13101.
 XX
 PT New nucleic acid encoding protein that increases neuronal cell
 PT proliferation - useful as nerve growth factor and for detection or
 PT inhibition of differentiation factors
 XX
 PS Claim 5; Page 17; 27pp; German.
 XX
 CC This sequence represents the human hsfz protein. This protein is found to
 CC increase the proliferation of neuronal cells. Such proteins can be used
 CC as nerve cell growth factors and for the detection and/or inhibition of
 CC differentiation factors, specifically those corresponding to the
 CC Drosophila melanogaster wingless or mouse int-1 type.
 XX
 SQ Sequence 325 AA;

Query Match 44.2%; Score 831; DB 19; Length 325;
 Best Local Similarity 50.8%; Pred. No. 4.3e-73;
 Matches 164; Conservative 52; Mismatches 77; Indels 30; Gaps 8;

QY 3 LSILVALCWLHVALGVGAPCAVRIKCRHMPWNIITRMPNHLHSTQENAILAEQYE 62
 Db 16 LLALALCL-LRVP-GARAAACEPVRIPLCKSLPMWNTKPNHLHSTQDNAILAEQFE 73
 QY 63 ELVDVNCVAVLREFFFCAMVAPICTLEFLHDPIKPCSVQCRARDCEPLMKMYNHWSPS 122
 Db 74 GLLGTHCSPDLLFLCAMPYAPICTIDFQHEPIKPCSVGERARQGCETILIKYRHSWPEN 133

QY 123 LACDELPPVDRGVCISPEAIVT---DLPEDVKWIDITPDMVQERPLDVCKRLSPDRCK 178
 Db 134 LACEELPPVDRGVCISPEAIVTADGADFMDSS-----NGNCRGASSERC 178
 QY 179 KCKVKPTLATYLSKNYSYVIHAKIKAVQSGGNEVTVVDVKEIFKSS-SPIRTOVPL 237
 Db 179 KCKPIRATQKTVFRNNYNYVIRAKVKEI-KTKCHDVAVVEVKEILKSSLVNIPROTVNL 237
 QY 238 IYNSSCQCQPHILPHQDVLIMCYEWRSMMLLENCLVEKWRDQLSKRSQWEERLQEQR 295
 Db 238 YTSSGCLCPLNVEEYIIMGYEDEKRSLLVEGSAIEKWKDRLGCKVKRMDMKLRHLIG 297
 QY 296 RTVQDKKKTAGTSTR-----SNP 313
 Db 298 LSKSDSSNSDSTQSQKSGRNSNP 320

RESULT 15
 AAW48694
 ID AAW48694 standard; Protein; 325 AA.
 AC AAW48694;
 XX
 DT 04-SEP-1998 (first entry)
 XX
 DE Bovine growth-inducing protein Frzb sequence.
 XX
 KW Frzb; growth-inducing protein; bovine; human; Xenopus; cartilage;
 KW bone; nerve; muscle; tumour; Wnt-expressing tumour; myodegeneration;
 KW subglottic stenosis; chondromalacia patellae; osteoarthritis;
 KW joint surface lesion; neurodegeneration; Alzheimer's disease;
 KW osteodegeneration; angiogenesis; wound healing.
 XX
 OS Bos sp.
 XX
 FH Key Location/Qualifiers
 FT Peptide 7..27
 FT /note= "putative signal peptide"
 FT Cleavage-site 32..33
 FT /note= "putative signal peptide cleavage site"
 FT Protein 33..325
 FT /note= "mature peptide"
 FT Domain 35..147
 FT /note= "N-terminal domain"
 FT Region 73..94
 FT /note= "putative transmembrane region"
 XX
 PN W09816641-A1.
 XX
 PD 23-APR-1998.
 XX
 PF 08-OCT-1997; 97WO-US18362.
 XX
 PR 20-MAR-1997; 97US-0822333.
 PR 11-OCT-1996; 96US-0729452.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Hoang B, Luyten FP, Moos M, Wang S;
 XX
 DR WPI: 1998-251288/22.
 DR N-PSDB; AAV18253.
 XX
 PT New nucleic acid encoding human, bovine and Xenopus Frzb protein -
 PT and related proteins, antibodies, peptide(s), vectors and
 PT transformed cells, used to induce growth of cartilage, bone, nerve
 PT and muscle, also for inhibiting Wnt-expressing tumours
 XX
 PS Claim 4; Fig 1; 66pp; English.
 XX
 CC This represents a bovine growth-inducing protein Frzb. Bovine, human
 CC and Xenopus Frzb genes which are shown in AAV18253 to AAV18255 are

CC related to the frizzled gene in Drosophila. The corresponding bovine,
CC human and Xenopus Frzb protein sequences are shown in AAW48694 to
CC AAW48696. A recombinant construct containing a Frzb encoding nucleic acid
CC linked to a heterologous promoter in an expression vector can be used to
CC produce recombinant Frzb proteins. The Frzb proteins may be formulated
CC with fibrin glue, freeze-dried cartilage grafts or collagen (optionally
CC also cartilage progenitor cells, chondroblasts or chondrocytes). They
CC are coated on to, or mixed with, a (non-)resorbable matrix, or mixed with
CC a biodegradable polymer. They modulate activity of the growth factors
CC Wnt-1 to 8. The Frzb proteins induce skeletal morphogenesis, embryonic
CC pattern formation and tissue specificity and are used to induce growth
CC of cartilage, bone, nerve and muscle, particularly in cases of
CC subglottic stenosis, chondromalacia patellae, osteoarthritis, joint
CC surface lesions, neurodegeneration (e.g. Alzheimer's disease),
CC myodegeneration or osteodegeneration. They also modulate Wnt-mediated
CC signalling in cells, and are used to inhibit growth of Wnt-expressing
CC tumours (particularly mammary or intestinal). The Frzb genes may also be
CC used to identify specific modulators or as a growth factor for cells of
CC the chondrocyte lineage in vitro, to stimulate wound healing, to promote
CC angiogenesis, to prevent transplant rejection and as adjunct to
CC chemotherapy or immunotherapy. Fragments of Frzb proteins are used for
CC detecting genetic abnormalities associated with Frzb genes.

XX Sequence 325 AA;

Query Match 44.2%; Score 831; DB 19; Length 325;
Best Local Similarity 51.4%; Pred. No. 4.3e-73;
Matches 166; Conservative 48; Mismatches 77; Indels 32; Gaps 8;

QY 3 LSLVALCLWLHLALGVRCAPEAVRIPMCRHMPNITRMPNHLHSTOENAILAEQYE 62
Db 16 LIALAALCL-LRVP-GARAAACEVRIPICKSLPNMTKMPNHLHSTOANILAEQFE 73
QY 63 ELVDVNCSAVLRFFFCAMVAPICTLEFLHDPKCKVCORARDCEPLMKMKNHWPES 122
Db 74 GLLTHCSPDLLFFLCAMVAPICTIDFQHEPKCKVCERARQCGCEPILIKYRHSWPES 133
QY 123 LACDELVPYDVGVCISPEAIVT- - - - -DLPEYKWKIDITPDMVMQERPLDVCCKRLSPDRC 178
Db 134 LACEELPYDVGVCISPEAIVTAGDAPDMDSS- - - - -NGNCRGASSERC 178
QY 179 KCKKVKPTLATYLSKNYSVIAKIKAVORSOCNEVTVVDVKEIFKSS-SPIPTQVPL 237
Db 179 KCKPVRAQTQTYFRNNYNVIRAKYKEI-KTKCHDVTAVVEVKEILKASLVNIPRETVAL 237
QY 238 ITNSSQCOPHILPHODVLIMCY--EWSRSMLENCLEKVRDOLSKRSIOWEERLQQR 295
Db 238 YTSGLCPPLVNWEEYLLMGYEDEERSKLLVEGSIAEKWKDRGLGKVKRWDMKLRHLG 297
QY 296 RTVQD- - - - -KKKTAGTSRS 311
Db 298 LNTSDSHSDSTQSQKPGRNSNS 320

Search completed: March 7, 2003, 11:23:56
Job time : 40 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	830	44.2	323	4	US-08-878-474-7		Sequence 7, Appli
2	828	44.1	325	4	US-08-878-474-9		Sequence 9, Appli
3	816	43.4	318	4	US-08-878-474-3		Sequence 3, Appli
4	338.5	18.0	585	4	US-08-937-067-9		Sequence 9, Appli
5	305	16.2	585	4	US-08-937-067-14		Sequence 14, Appli
6	298.5	15.9	572	4	US-08-937-067-13		Sequence 13, Appli
7	293	15.6	565	4	US-08-937-067-8		Sequence 8, Appli
8	263.5	14.0	666	4	US-08-937-067-10		Sequence 10, Appli
9	255	13.6	537	4	US-08-937-067-11		Sequence 11, Appli
10	248	13.2	295	4	US-08-893-654B-6		Sequence 6, Appli
11	232.5	12.4	281	4	US-08-893-654B-2		Sequence 2, Appli
12	228.5	12.2	280	4	US-08-893-654B-4		Sequence 4, Appli
13	228	12.1	314	4	US-08-937-067-7		Sequence 7, Appli
14	220	11.7	706	2	US-08-987-289-2		Sequence 2, Appli
15	218	11.6	295	4	US-08-937-067-2		Sequence 2, Appli
16	215.5	11.5	709	4	US-08-937-067-12		Sequence 12, Appli
17	207	11.1	317	4	US-08-937-067-6		Sequence 6, Appli
18	199.5	10.6	212	4	US-08-937-067-4		Sequence 4, Appli
19	149.5	8.0	641	4	US-09-233-989-10		Sequence 10, Appli
20	110	5.9	787	4	US-08-720-484A-4		Sequence 4, Appli
21	110	5.9	787	4	US-08-953-823A-4		Sequence 4, Appli
22	110	5.9	787	4	US-09-398-239-4		Sequence 4, Appli
23	107	5.7	793	2	US-08-720-484A-2		Sequence 2, Appli
24	107	5.7	793	4	US-08-953-823A-2		Sequence 2, Appli
25	107	5.7	793	4	US-09-293-505-16		Sequence 16, Appli
26	107	5.7	793	4	US-09-293-505-17		Sequence 17, Appli
27	107	5.7	793	4	US-09-398-239-2		Sequence 2, Appli

Db 29 ASCEPVRIIPCKMSPMNMTKMPNHLHSHSTQANAIIAIEOFEGLLTQESQDILLFLCAMY 88
QY 82 APICTELEFLHDPIKCKSVQCORADCEPLMKMYNHSWPESLACDPELPYDRGVCSPEA 141
Db 89 APICITDQHEPIKCKSVQCORADCEPLMKMYNHSWPESLACDPELPYDRGVCSPEA 148
QY 142 IVTDLPEVDKWDITPDMVMQBRPLDVCCKRLSPDRCKCKYKPTLATYLSKNYSYVHA 201
Db 149 IVT----VEQGTDSMPDFSDMSNNGSGR---EHCKCKPKMKATOKTYLKNYNYVIRA 201
QY 202 KIKAVORSCEVNTVVDVKEIFKSS-SPIPRTQVPLTNSSCQCPHILPHQDVLIMCYE 260
Db 202 KIKAVORSCEVNTVVDVKEIFKSS-SPIPRTQVPLTNSSCQCPHILPHQDVLIMCYE 260
QY 261 --WRSRMLENCLEVKWRDQLSKRSIOWEERLQEBORRTVQDKKTKTAGRTSRNPPKPG 318
Db 261 DKERTRELLIVEGSLAEKWRDLRAKKVRWDQKLRR-----PRKSK 300
QY 319 KPPAPKPPSKNRIKTRSAO 338
Db 301 DPVAP---IPNKNNSNSROAR 317

RESULT 4

US-08-937-067-9
; Sequence 9, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuel
; APPLICANT: Melkonian, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; . TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; . TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-937-067-9

Query Match 18.0%; Score 338.5; DB 4; Length 585;
Best Local Similarity 33.3%; Pred. No. 3e-25;
Matches 73; Conservative 37; Mismatches 84; Indels 25; Gaps 6;

QY 5 ILVALCLWLHLALGVNGAP-CEAVRIPMCRHMPNITRPNHLHSHSTQANAIIAIEOFEGLLTQESQDILLFLCAMY 63
Db 13 LLLLAQLVGRAAAASKAPVCQETVPMCRIGYNTLTHMPNQFNHDTQDEAGLEVHGFWP 72

QY 64 LVDVNCASVLRFFFCAMVAPICTLEFLHDPIKCKSVQCORADCEPLMKMYNHSWPESL 123
Db 73 LVEIQCSPLRFFLCMTWYPTICLPDY-HKPLPCKSVQCORAGKAGCSPLMRQYGFAMPERM 131
QY 124 ACDELFPVYDRGVCSISPEAIVTDLPEVDKWDITPDMVMQBRPL-----DVEDCKRL 173
Db 132 SCDRLPVLGR-----DAEVLCDMYNSEATTAPPRPPAKPTLPGPCAPASGGBCPAG 185
QY 174 SPDRCKCKK-VKPTLATYLSKNYSYVHAHAKIKAVQBSGC 211
Db 186 GPFVCKCKRPFVFPIL-----KESHPLYNKVKTGVQVPC 218
RESULT 5
US-08-937-067-14
; Sequence 14, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuel
; APPLICANT: Melkonian, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; . TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; . TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-937-067-14

Query Match 16.2%; Score 305; DB 4; Length 685;
Best Local Similarity 39.5%; Pred. No. 7.9e-22;
Matches 58; Conservative 31; Mismatches 46; Indels 12; Gaps 5;

QY 4 SILVALCLWLHLALGVNGA-----PCEAVRIPMCRHMPNITRPNHLHSHSTQANAIIA 58
Db 11 SLAALAV-LQRSSGAAASAKELACQETVPLCKIGYNTYMPNQFNHDTQDEAGLEV 69
QY 59 EQYEELVDVNCASVLRFFFCAMVAPICTLEFLHDPIKCKSVQCORADCEPLMKMYNHS 118
Db 70 HQFWPLVEIQCSPLDKKFLCISMTYPTIC-LDYKKPLPCKSVQCORAGKAGCAPLMROYGFA 128
QY 119 WPESLACDELFPYDRGVCSISPEAIVTD 145
Db 129 WPDWRMCRDLP--EQG---NPDTLCMD 150

RESULT 7
 US-08-937-067-8
 ; Sequence 8, Application US/08937067
 ; Patent No. 6433155
 ; GENERAL INFORMATION:
 ; APPLICANT: Umansky, Samuil
 ; APPLICANT: Melkonyan, Hovsep
 ; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
 ; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: CA

```

RESULT 8
US-08-937-067-10
: Sequence 10, Application US/08937067
: Patent No. 6433155
: GENERAL INFORMATION:
: APPLICANT: Umansky, Samuill
: APPLICANT: Melkonyan, Hovsep
: TITLE OF INVENTION: A FAMILY OF GENES ENCODING
: TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES;
: TITLE OF INVENTION: METHODS OF USE THEREOF
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/937,067
: FILING DATE:
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Lehnhardt, Susan K.

```



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;
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 666 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-937-067-10

Query Match 14.0%; Score 263.5; DB 4; Length 666;
Best Local Similarity 36.3%; Pred. No. 1e-17;
Matches 62; Conservative 30; Mismatches 52; Indels 27; Gaps 8;

QY 11 LW-LHLALGVGA-----PCEAVRIPMCRHMPWNITRPNHLHHSQTQENAILATEQYEELV 65
Db 10 LWLLTVLFGQIGGHSLSFCEPITLRMCQDLPLYNTTTPNPNLLNHYDQQTAAALAMEPFPWV 69

QY 66 DVNCSAVLRAFFFCAMVAPICITLFLHDPKPKCKSVCORADDCCEPLMKMYNHSWPESLAC 125
Db 70 NLDCSRDFRFLCALYAPIC-MEYGRVTL-PCRRLCORAYSCSKLWEMFGVWPFVWPEDEMC 127

QY 126 DELP-----VYDRGVCI-----SPEAIVTD-----LPEDVKWIDITPDM 159
Db 128 SRFPDCEPYRLVLDNLVCDPTEGAPVAVORDYGFWCPELX---IDPL 175

RESULT 9
US-08-937-067-11
; Sequence 11, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuel
; APPLICANT: Melkonian, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 537 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-937-067-11
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```
Query Match 13.6%; Score 255; DB 4; Length 537;
Best Local Similarity 27.2%; Pred. No. 5.2e-17;
Matches 69; Conservative 49; Mismatches 110; Indels 26; Gaps 7;

QY 3 LSLVALCLWLHALGV---RGAPCEAVRIPMCRHMPWNITRPNHLHHSQTQENAILATE 59
Db 21 LGLLLQFLLLRPTLGLFGDEEERRCDPIRIAMCONLGYNVTKMPNLVGLHQLQDAELQLT 80

QY 60 OYEELVDVNCSAVLREFFCAMVAPICITLFLHDPKPKCKSVCORADDCCEPLMKMYNHSW 119
Db 81 TFTPPLIQYGCSSQLQFLCSVYVPMCT-EKINIPICPGCMGUSVRRRCRCPVLUREGFAW 139

QY 120 PESLACDELPPYD--RGVCTISPEAIVTDLPEDVKWIDITPDMVQBRPLDVCCKRLSPDR 177
Db 140 PDTLNSCKFPONDHNHMCMEGPG-----DEEYPLPKTPIOPGEE-----CHSVCSNS 188

QY 178 CKCKKVKPTLTYLSKNYSYVIHAKI-----KAVORSGCNEVTYVDVVKEIFKSSSP 229
Db 189 DQYIWKRSINCLVLCGCGYDAGLYSRSAKETDIWMAVWASLC-FISTTFTVLFLIDSSR 247

QY 230 IPTQVPLITNSSC 243
Db 248 FSYPERPIIFLSMC 261

RESULT 10
US-08-893-654B-6
; Sequence 6, Application US/08893654B
; Patent No. 6165748
; GENERAL INFORMATION:
; APPLICANT: RACIE, LISA, ET ALIA
; TITLE OF INVENTION: Frazzled NUCLEOTIDE SEQUENCES,
; TITLE OF INVENTION: EXPRESSION PRODUCTS, COMPOSITIONS AND USES
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGE PARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140-2387
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,654B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MEINERT, M.C.
; REGISTRATION NUMBER: 31,544
; REFERENCE/DOCKET NUMBER: G1 5279
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498 8574
; TELEFAX: 617 876 5851
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-893-654B-6

Query Match 13.2%; Score 248; DB 4; Length 295;
Best Local Similarity 25.4%; Pred. No. 1.1e-16;
Matches 80; Conservative 48; Mismatches 109; Indels 78; Gaps 14;

QY 5 ILVALCLWLHALGV-----GAPCEAVRIP-----MCRHMPWNITRPNHLHHSQTQEN 53
Db 13 LIVLLCF---LACGSGSMYLDFFGSSSRMRIPKSMALCYDIGYSEMRIPNLLHETMAE 69
```


Qy	242	SCQCPHILPHQDVLIMC-----YEWRSRMLLENCLVEKWR	277
		: : : : : :	
Db	229	NCAOKLIRNRPTVYVIAGDIHHGKVKNRVFHWOKDSOL-TLATRRWR	276

RESULT 13

US-08-937-067-7
; Sequence 7, Application US/08937067
; Patent No. 6433155

GENERAL INFORMATION:

APPLICANT: Umansky, Samuel
 APPLICANT: Melkonian, Hovsep
 TITLE OF INVENTION: A FAMILY OF GENES ENCODING
 TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
 TITLE OF INVENTION: METHODS OF USE THEREOF
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1019
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/937,067

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Lennhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-937-067-7

Query Match 12.1%; Score 228; DB 4; Length 314;
Best Local Similarity 26.3%; Pred. No. 1.2e-14;
Matches 72; Conservative 45; Mismatches 107; Index

Qy	23	PCBAVRIP----	MCRIWPNWITRMPNHLHHSTQENAILAEIQEYEEVLVDVNCSAVLRFECF	78
Db	55	PPQCVDPADRLRCHNNGYKKWLPVLP	LEHETMAEYKQOASSVPLLNKKNCHAGTQVFIC	114
Qy	79	AMVAPICTLEFLDPTKPKCSVCORARDCE	PLMKWNHNSWPESLACDELPIYDRCVGCT	138
Db	115	SLFAPVC----	LDRPIYPCWNLCEAVRDSCEPVQFGFYWPBMLKCDRPEGD--	168
Qy	139	---PEALVTDLPEVKNWIDITPOMMYOER	PLVDVCKRLSPDRCKCKVKVKTPTATYLSKNY	195
Db	169	MTPPNTEASKPOCT--	TCPV-----PCDNELK-----SEATIEHLCAS-	205
Qy	196	SYVIHAKIKAVORGSGNEVTTVDVKEIF	KSSSPIRTPQVP-----LIINSSCQCCHI--	248
Db	206	EPALRMKIKEVKKE--	NGDKKIYPKKKKPKLGPINKKDLKLVLKNGACDPCPCHOLDN	263
Qy	249	LPHQDVLIMCYEWRSRMMLLENCLVEK	WRDQLSK	282
Db	264	LSHH--FLIMGRKVKSOYLL---	TAIHKW-DKKNK	292

RESULT 14

US-08-987-289-2 ; Sequence 2, Application US/08987289
: Patent No. 5994098

: GENERAL INFORMATION:

```

APPLICANT: HU, EDLING
APPLICANT: ZHU, YUAN
TITLE OF INVENTION: A Human 7-TM Receptor Similar
TITLE OF INVENTION: to Murine Frizzled-6 gene
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,289
FILING DATE: 09-DEC-1997

```

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; CLASSIFICATION:
;
; REPORT APPLICATION DATA:

```

PRIOR APPLICATION DATA: 60/048,725
 FILING DATE: 02-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: PRESTIA, PAUL F
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GH-70060
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0701
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 706 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-987-289-2

Query Match 11 78. Score 220. DB 2. Length 706.

Query Match 11.7%; Score 220; DB 2; Length 1700;
Best Local Similarity 31.9%; Pred. No. 2.3e-13;
Matches 44; Conservative 27; Mismatches 63; Indels 4; Gaps 3;

Qy	1	MFLSILVALCLWLHLALGVRCACEAVRIPDCWRHMPNNITRPMNHLHHSTQENALAEQ	60
Db	3	MTELLT--CIFLLKGLHSFTCEPTIVPRCKMKYNTFTFPLMGHYDQSTAAVEMEH	60
Qy	61	YEELVDNCSAVLRFFFCAMYPACTLLEFLHDPKPKCSVCQARDDCEPLMKMYNHSWP	120
Db	61	FLPLANECSPNIEFTFCKAFVPTC-IEQH-VVPPCKKLCEKVISDCKKLIDTFGIRWP	118
Qy	121	ESLACDELPPVYDGVGCIS	138
Db	119	EELCDRLLOYCDETPVPT	136

RESULT 15

RESOLUT 13
US-08-937-067-2
; Sequence 2, Application US/08937067
: Patent No 6433155

```

:
:
: GENERAL INFORMATION:
:
: APPLICANT: Umansky, Samuil
:
: APPLICANT: Melkonyan, Hovsep
:
: TITLE OF INVENTION: A FAMILY OF GENES ENCODING
:
: TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES
:
: TITLE OF INVENTION: METHODS OF USE THEREOF
:
:

```

; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
 ; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
 ; TITLE OF INVENTION: METHODS OF USE THEREOF

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 7, 2003, 11:21:34 ; Search time 20 Seconds
(without alignments)
1663.126 Million cell updates/sec

Title: US-09-909-775-2
Perfect score: 1879
Sequence: 1 MFLSILVALCLWLHLALGVR.....SPKKNIKTRSAQKRTNPKRV 346
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1033	55.0	197	JC7735	frizzled-related p
2	319	17.0	694	S71786	wingless receptor
3	300.5	16.0	647	JF0337	Frizzled-1 protein
4	300	16.0	641	A45054	probable intercell
5	298.5	15.9	574	JF0339	Frizzled-7 protein
6	293	15.6	565	JF0338	Frizzled-2 protein
7	289	15.4	581	S03540	gene frizzled prot
8	283	15.1	568	T25162	Frizzled-1 protein
9	282	15.0	581	JC7086	FZD10 protein - hu
10	279	14.8	550	T37325	wingless protein r
11	265	14.1	537	JC7127	frizzled protein 4
12	262.5	14.0	666	JC7312	frizzled-3 protein
13	226.5	12.1	605	T31690	hypothetical prote
14	220	11.7	706	JF0164	frizzled-6 protein
15	218	11.6	295	JF0174	frizzled protein-2
16	207	11.0	317	JF0175	frizzled protein-1
17	204	10.9	1113	JF0315	low-density lipopr
18	162	8.6	579	JC7629	membrane-type friz
19	149	7.9	1774	T B56101	collagen alpha 1(X
20	120.5	6.4	526	T13484	frizzled protein h
21	107	5.7	400	T46383	hypothetical prote
22	107	5.7	3488	T34418	hypothetical prote
23	106.5	5.7	651	T21175	hypothetical prote
24	105	5.6	793	JC5539	Smoothed protein
25	103.5	5.5	965	S62935	hypothetical prote
26	98.5	5.2	492	F86384	probable protein f
27	96.5	5.1	581	B54665	netrin-2 precursor
28	96.5	5.1	1483	T E80143	F6F3.12 protein -
29	94.5	5.0	606	A54665	netrin-1 precursor

30	94	5.0	859	2	T38168	hypothetical prote
31	94	5.0	6642	2	T29757	protein UNC-89 - C
32	92.5	4.9	1346	2	A57376	probable regulator
33	92	4.9	422	2	T39306	mitogen-activated
34	91.5	4.9	686	2	S70180	chomataxis protein
35	91	4.8	1104	2	T38869	transcription fact
36	91	4.8	1151	1	S45390	protein kinase C (
37	91	4.8	1201	2	T29329	hypothetical prote
38	90.5	4.8	261	2	A30337	probable AraC-fam
39	90.5	4.8	669	2	AB3103	cell surface recep
40	90.5	4.8	960	2	JF0356	gamma-aminobutyric
41	90	4.8	591	2	T48141	acroganin - guine
42	90	4.8	1637	2	T00070	hypothetical prote
43	89.5	4.8	237	2	AH0207	Prop effector homo
44	89.5	4.8	497	2	T52308	very-long-chain fa
45	89.5	4.8	1030	2	T18374	B-cell receptor pr

ALIGNMENTS

RESULT 1

JC7735
frizzled-related protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 14-Dec-2001
C:Accession: JC7735
R:Yam, J W P.; Chan, K W.; Wong, V K W.; Hsiao, W L W.
Biochem. Biophys. Res. Commun. 286, 94-100, 2001
A:Title: Transcriptional activity of the promoter region of rat frizzled-related prot
A:Reference number: JC7735; MUID:21378144; PMID:11485313
A:Accession: JC7735
A:Molecule type: DNA
A:Residues: 1-197 <YAM>
A:Cross-references: GB:AF140347
C:Comment: This protein is a new family of secreted proteins involved in tumorigenesi
C:Genetics:
A:Gene: rFrp
A:Introns: 148/3; 175/3

Query Match 55.0%; Score 1033; DB 2; Length 197;
Best Local Similarity 94.9%; Pred. No. 1.8e-76;
Matches 187; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY	1	MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHSTQENAILAIEQ	60
Db	1	MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHSTQENAILAIGQ	60
QY	61	YEELVDVNCSSVLSFFLCAMYPICITLEFLHDPKPKSVQCARDDCEPLMKMYNHSWP	120
Db	61	YEELVDVNCSSVLSFFLCAMYPICITLEFLHDPKPKSVQCARDDCEPLMKMYNHSWP	120
QY	121	ESLACDELVYDRGVCISPEAIVTDLPEDVKWIDITPDMVQRPDLVDCKRLSPDRCK	180
Db	121	ESLACDELVYDRGVCISPEAIVTDLPEDVKWIDITPDMVQRPDLVDCKRLSPDRCK	180
QY	181	KKVKPTLATYLSKNYSY	197
Db	181	KKVKPTLATYLSKNYSY	197

RESULT 2

S71786
wingless receptor precursor dfz2 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 02-Mar-2001
C:Accession: S71786; S78444
R:Bhanot, P.; Brink, M.; Harryman Samos, C.; Hsieh, J.C.; Wang, Y.; Macke, J.P.; And
Nature 382, 225-230, 1996
A:Title: A new member of the frizzled family from Drosophila functions as a wingless
A:Reference number: S71786; MUID:96353971; PMID:8717036
A:Accession: S71786
A>Status: nucleic acid sequence not shown

A: residues: 1-416, 'T', 418-694 X2
A: cross-references: EMBL:U65589; NID:g1518050; PIDN:AC47273.1; PID:g1518051
C:genetics:
A:gene: dfz2
A:cross-references: FlyBase:FBgn0016797
C:superfamily: fruit fly frizzled protein
C:keywords: transmembrane protein

QY 29 IPMCRIMPWNITRMPNHLHSTQENAILAIEQYEELVDVNCNSAVLRFFFCMYA
 116 IPLCTDAYNOTIMPNLNIGHTNOEDAGLEVHGYPLVKVOCSAELKFFELCSMYA

QY 89 FLHDPKPKSVQCRRARDCEPLMKMYNHSWPSLACDELPVYDRG-VCI 137
— : |||:|||| : ||| : |||:||| : ||| :

Dd 175 -LEQLPPCRSLCERAQ-GCEALMNKEFGWPDTLKCEKFVPHVGELCV 222

Biochem. Biophys. Res. Commun. 252, 117-122, 1998
 A:Title: Molecular cloning, differential expression, and chromosomal localization of
 A:Reference number: JE0337; MUID:99032814; PMID:9813155
 A:Accession: JE0339
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-574 <SAG>
 A:Cross-references: DDBJ:AB017365; NID:G3927886; PIDN:BA034668.1; PID:G3927887
 C:Superfamily: fruit fly frizzled protein

OY 84 ICTLEFLHDPKPKCKSVQCARDDCEPLMKMYNHSWPESLACDELPPVDRG-VCI 137
 :||: | | ||:|:|||| || | | | | | | | | | | | | | | | | | |
Dp 109 VCTV--LDQAIPCKSLICERAROGCEALMNKEGFOWPERLCENFPFHGAIECV 161

RESULT 6
JE0338
Frizzled-2 protein - human
C:Species: Homo sapiens (man)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Mar-2001
C:Accession: JE0338

Biochem. Biophys. Res. Commun. 252, 117-122, 1998
 A:Title: Molecular cloning, differential expression, and chromosomal localization of
 A:Reference number: JE0337; MUID:99032814; PMID:9813155
 A:Accession: JE0338
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-565 <SAG>
 A:Cross-references: DDBJ:AB017364; NID:G3927884; PIDN:BAA34667.1; PID:G3927885
 C:Superfamily: fruit fly frizzled protein

RESULT 10

T37325
wingless protein receptor Cfz2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Mar-2001
C:Accession: T37325
R:Sato, A.; Kojima, T.; Uti-Tel, K.; Miyata, Y.; Saigo, K.
Development 126, 4421-4430, 1999
A:Title: Dfrizzled-3, a new Drosophila Wnt receptor, acting as an attenuator of Wingless
A:Reference number: Z21689; MUID:10498678
A:Accession: T37325
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-550 <SAT>
A:Cross-references: EMBL:AB026113; NID:g5931529; PIDN:BAA84678.1; PID:g5931530
C:Genetics:
A:Gene: Cfz2
A:Superfamily: fruit fly frizzled protein
C:Keywords: receptor; signal transduction; transmembrane protein

Query Match 14.8%; Score 279; DB 2; Length 550;
Best Local Similarity 30.7%; Pred. No. 7.9e-15;
Matches 75; Conservative 32; Mismatches 89; Indels 48; Gaps 9;

QY 1 MFLSILVALCLWLHLAGVRGA-----PCEAVRIPMCRHMPNITRMPNHLHSTOENA 54

DB 1 MLRLISV-----LFLLLSGCALFGKQKEQITPLCKGIGYNWTFSPNSYCHEKQEEA 55

QY 55 ILAIEQYBELVDVNCSSAVLRFFFCAMVAPICTLEFLHDPKPKSVQCORARDCEPLMKM 114

DB 56 GLEVHGFYPLVEVGCFOHLKFFLECTWYTPICQ-ENYDKPILPOMELCVEARSKCSPIMAK 114

QY 115 YNHSWPESLACDELPE-----VYDRGVCISPEAIVTDLPE-----EDVFW 152

DB 115 YGRWPETLSCEALPKMSQDMSTGNTCAAP-----PDPKQKHGHHKNNQNNQNHNY 170

QY 153 IDITPMVMQERPLDVCCKRSLDRCKCKVKP--TLATVLSK-----NYSYVIHAKIKA 205

DB 171 SPDGPEVGSKIDNEVIA---GPSEQCQTCNQPFQVASEKSKVGNVTNCAYSCHSPALA 227

QY 206 VORS 209

DB 228 ESHS 231

RESULT 11

JC7127
frizzled protein 4 - human
C:Species: Homo sapiens (man)
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
C:Accession: JC7127
R:Kirikoshi, H.; Sagara, N.; Kolke, J.; Tanaka, K.; Sekihara, H.; Hirai, M.; Katoh, M.
Biochem. Biophys. Res. Commun. 264, 955-961, 1999
A:Title: Molecular cloning and characterization of human frizzled-4 on chromosome 11q14-
A:Reference number: JC7127; MUID:20012777; PMID:10544037
A:Accession: JC7127
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-537 <KIR>
A:Cross-references: GB:AB032417; DBJ:AB032417; NID:g6277265; PID:g6277266
C:Genetics:
A:Gene: FZD4
A:Map position: 11 region q14 - q21
A:Superfamily: fruit fly frizzled protein

Query Match 14.1%; Score 265; DB 2; Length 537;
Best Local Similarity 28.7%; Pred. No. 1e-13;
Matches 74; Conservative 47; Mismatches 107; Indels 30; Gaps 8;

QY 3 LSLVALCLWLHLAGVRG-----APCEAVRIPMCRHMPNITRMPNHLHSTOENAI 55

DB 3 LSLVALCLWLHLAGVRG-----APCEAVRIPMCRHMPNITRMPNHLHSTOENAI 55

DB 17 VGLSLGLLLQLLLLLLPARGFGDEERRRCDPTRISMCQNLGYNVTMPNVLVGHLEQTDAE 76

QY 56 LAIEQYBELVDVNCSSAVLRFFFCAMVAPICTLEFLHDPKPKSVQCORARDCEPLMKM 115

DB 77 LQLTTTPTLIQYCCSLOLFFLGSVVVPMCT-EKINIPGCGMCLSVKRRCEPVLPKEF 135

QY 116 NHSWPESLACDELPEVVD--RGVCISPEAIVTDLPEVDKVIDITPDMVMQERPLDVCCKRL 173

DB 136 GFAPESLNCCKRPFPQNDHNMCMGPG-----DEEVPLPKPTIQPGEE-----CHSV 184

QY 174 SPDRCKCKVKPTLATYLSKNYSYVIHAKI-----KAVORSQGCNEVTTVVVDVKEIFK 225

DB 185 GTNSDQYIWKSLNCLVLCQDGYDSRAKEFTDINMAVWASLC-FISTAFTVLTFLI 243

QY 226 SSSPIPTQVPLITNSSC 243

DB 244 DSRFSYPERPIFLSMC 261

RESULT 12

JC7312
frizzled-3 protein - human
C:Species: Homo sapiens (man)
C:Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 02-Mar-2001
C:Accession: JC7312
R:Sala, C.F.; Formenti, E.; Terstappen, G.C.; Caricasole, A.
Biochem. Biophys. Res. Commun. 273, 27-34, 2000
A:Title: Identification, gene structure, and expression of human frizzled-3 (FZD3).
A:Reference number: JC7312
A:Accession: JC7312
A:Molecule type: mRNA
A:Residues: 1-666 <SALA>
A:Cross-references: GB:AJ27242
A:Experimental source: brain
C:Comment: This protein, a seven-transmembrane receptor belonging to the frizzled fam
nositol levels in cells.
C:Genetics:
A:Gene: fzd3
A:Map position: 8p21
A:Superfamily: fruit fly frizzled protein
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 14.0%; Score 262.5; DB 2; Length 666;
Best Local Similarity 34.9%; Pred. No. 2.1e-13;
Matches 61; Conservative 32; Mismatches 55; Indels 27; Gaps 8;

QY 7 VALCLW-LHLALGVRCG----PCEAVRIPMCRHMPNITRMPNHLHSTOENAILAIEQY 61

DB 6 IVPSLWPLTVPMGHIGGHSLSFCEPITLRMCQDLPTNTTFMPNLLNHYDQOTAAALAMEPP 65

QY 62 EELVDVNCSSAVLRFFFCAMVAPICTLEFLHDPKPKSVQCORARDCEPLMKMYNHSWPE 121

DB 66 HPWNLDGSRDFPFICALYAPIC-MEYGRVTL-PCRRLCQRAYSCSKLMENFGVPWPE 123

QY 122 SLACDELPE----VYDRGVCI-----SPEAIVTD----LPEDYKVIDITPDM 159

DB 124 DMESCRFPDCEPYPRLDVNLNLAGETEGAPVAVQRDYGVCPCRELK---IDPDL 175

RESULT 13

T31690
hypothetical protein F27E11.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 02-Mar-2001
C:Accession: T31690
R:Wamsley, P.; Keppler, D.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid F27E11.
A:Reference number: Z21069
A:Accession: T31690
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-605 <WAM>

A:Cross-references: EMBL:AF016413; PIDN: AAB65257.1; GSPDB:GN00023; CBSP:F27E11.3
A:Experimental source: strain Bristol N2; clone F27E11

C:Genetics:

A:Gene: CESP:F27E11.3

A:Map position: 5

A:Introns: 28/3; 454/1; 520/1; 562/1

C:Superfamily: fruit fly frizzled protein

Query Match 12.1%; Score 226.5; DB 2; Length 605;
Best Local Similarity 29.5%; Pred. No. 1.6e-10;
Matches 59; Conservative 27; Mismatches 77; Indels 37; Gaps 7;

QY 39 ITRMNLHSHSTQENAILAIEQYEEELVDVNCASVLRFFFCAMYPICITLFLHDPKPKCK 98

Db 1 MTSFNSYGHGEQEEAGLEVHQFYPLVEVGCFOHLKFFLCTWYTIQY-ENYDKPILPCM 59

QY 99 SVCORARDCEPLMKMNHNSWPESLACDELP-----VYDRGVCI SPEAIVTDLP----- 147

Db 60 ELCVEARSKCSPIMAKYGRWPETUSCEALPKMSDOMSTGNICAAP----PDPKKQKHG 115

QY 148 -----EDVKWIDITPDMVQERPLVDCKRLSPDRCKKVKP--TLATYLSK- 193

Db 116 HHHKQNNQNNHNSYDPGPEVGISKIDNEVIA---GFSECOCTCNQPFQFVASEKSKV 172

QY 194 ----NYSYVIHAKIRAVQRS 209

Db 173 GNVNTCAVSCSPALAESHS 192

RESULT 14

frizzled-6 protein precursor - human

C:Species: Homo sapiens (man)

C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 02-Mar-2001

C:Accession: JE0164

R:Tokuhara, M.; Hirai, M.; Atomi, Y.; Terada, M.; Katoh, M.

Biochem. Biophys. Res. Commun. 243, 622-627, 1998

A:Title: Molecular cloning of human frizzled-6.

A:Reference number: JE0164; MUID:98153814; PMID:9480858

A:Accession: JE0164

A:Molecule type: mRNA

A:Residues: 1-706 <TO>

A:Cross-references: GB:AB012911; NID:g3062802; PIDN:BA25686.1; PID:g3062803

C:Comment: This protein is receptor for selected glycoproteins in development and carcin

C:Genetics:

A:Gene: Hfz6

A:Map position: 8q22.3-q23.1

C:Superfamily: fruit fly frizzled protein

C:Keywords: glycoprotein

F:1-18/Domain: signal sequence #status predicted <SIG>

F:201-222/Domain: transmembrane #status predicted <TM1>

F:233-255/Domain: transmembrane #status predicted <TM2>

F:281-312/Domain: transmembrane #status predicted <TM3>

F:324-345/Domain: transmembrane #status predicted <TM4>

F:370-393/Domain: transmembrane #status predicted <TM5>

F:417-436/Domain: transmembrane #status predicted <TM6>

F:473-495/Domain: transmembrane #status predicted <TM7>

F:38.352/Binding site: carbohydrate (Asn) #status predicted

Query Match 11.7%; Score 220; DB 2; Length 706;

Best Local Similarity 31.9%; Pred. No. 6.4e-10;

Matches 44; Conservative 27; Mismatches 63; Indels 4; Gaps 3;

QY 1 MFLSLVALCLHLALVGRGAPCEAVRIPMCRHMPNITRPNHLHSHSTQENAILAIEQ 60

Db 3 MFTFLT--CIFPLLRGHSLTCTCPITVPRCKMKWAYNMFTFPNLMGHYDQSIAAVEMEH 60

QY 61 YEELDVNCSAVLRFFFCAMYPICITLFLHDPKPKCKVCORARDDCEPLMKMNHNSWP 120

Db 61 FLPLANLECSPIETFLCKAFVPTC-IEQIH-VVPCPKLCEKYSVSDCKKLIDTFGIRWP 118

QY 121 ESLACDELPEYDRGVCIIS 138

Db 119 EELECDRLQYCDETVPVT 136

RESULT 15

frizzled protein-2 - human

C:Species: Homo sapiens (man)

C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999

C:Accession: JE0174

R:Hu, E.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Bealey, L.; Brooks, D.

Biochem. Biophys. Res. Commun. 247, 287-293, 1998

A:Title: Tissue restricted expression of two human frzbs in preadipocytes and pancrea

A:Reference number: JE0174; MUID:98308108; PMID:9642118

A:Accession: JE0174

A:Molecule type: mRNA

A:Residues: 1-295 <HUA>

C:Genetics:

A:Map position: 4q

Query Match 11.6%; Score 218; DB 2; Length 295;

Best Local Similarity 26.3%; Pred. No. 3.4e-10;

Matches 62; Conservative 41; Mismatches 91; Indels 42; Gaps 9;

QY 6 LVALCLWLHLALG-----VRGAPCEAVRIPMCRHMPNIT-----TRMPNHLHHS 49

Db 8 LLLFLASHCHCLGSARGLEFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHE 67

QY 50 TOENAILATEQYEEELVDVNCASVLRFFFCAMYPICITLFLHDPKPKCKVCORARDDCE 109

Db 68 TMKEVLEQAGAWIPLVMKCHDPTKFLGSLFAPVC-LOOLDETIQPCHSLCQVVKDRCA 126

QY 110 PLMKMNHNSWPESLACDELPEYDRGVCI SPEAIVTDLPEDVKWIDITPDMVQERPLDVD 169

Db 127 PVMSAFGFPWDMLECDRFP-QDNLDLCIPLASSDHLLP-----ATEAPKVC 173

QY 170 -CKRLSPD-----RCKCK-----KVKPTLATYLSKNYSYVIHAKIKAVOR-SCNE 213

Db 174 ACKNKNDNDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVGSE 229

Search completed: March 7, 2003, 11:25:27

Job time : 23 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2003, 11:20:34 ; Search time 13 Seconds
(without alignments)
1103.908 Million cell updates/sec

Title: US-09-909-775-2

Perfect score: 1879

Sequence: 1 MFLSLVALCLWLHLALGVR.....SPKNIKTRSAOKRTNPKRV 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	831	44.2	325	1 FRZB_BOVIN	Q95117 bos taurus
2	830	44.2	323	1 FRZB_MOUSE	P97401 mus musculus
3	828	44.1	325	1 FRZB_HUMAN	Q92765 homo sapien
4	338.5	18.0	585	1 FZD5_HUMAN	Q13467 homo sapien
5	331	17.6	577	1 FZD5_MOUSE	Q9eqd0 mus musculus
6	318	16.9	694	1 FR22_DROME	Q9vwx3 drosophila
7	312	16.6	591	1 FZD8_HUMAN	O00144 homo sapien
8	310	16.5	592	1 FZD9_MOUSE	Q9r216 mus musculus
9	308.5	16.4	549	1 FZD7_XENLA	Q9pkh8 xenopus lae
10	308	16.4	694	1 FZD8_HUMAN	Q9h461 homo sapien
11	307.5	16.4	642	1 FZD1_MOUSE	O70421 mus musculus
12	306	16.3	567	1 FZD7_CHICK	O57329 gallus gall
13	306	16.3	581	1 FZD8_XENLA	O93274 xenopus lae
14	305.5	16.3	592	1 FZD1_CHICK	O57328 gallus gall
15	305	16.2	685	1 FZD8_MOUSE	Q61091 mus musculus
16	303	16.1	559	1 FZD1_XENLA	Q919m5 xenopus lae
17	301.5	16.0	559	1 FZD5_XENLA	P58421 xenopus lae
18	300.5	16.0	648	1 FZD1_HUMAN	Q9u338 homo sapien
19	299.5	15.9	574	1 FZD7_HUMAN	O9u338 homo sapien
20	299	15.9	583	1 FR12_DROVI	Q24760 drosophila
21	298.5	15.9	572	1 FZD7_MOUSE	Q61090 mus musculus
22	294	15.6	641	1 FZD1_RAT	Q08463 rattus norv
23	293.5	15.6	551	1 FZD2_XENLA	Q9puu6 xenopus lae
24	293.5	15.6	580	1 FZD8_XENLA	Q9w742 xenopus lae
25	293	15.6	565	1 FZD2_HUMAN	Q14332 homo sapien
26	293	15.6	570	1 FZD2_MOUSE	Q9jip6 mus musculus
27	293	15.6	570	1 FZD2_RAT	Q08464 rattus norv
28	292	15.5	585	1 FZD1_CHICK	Q9pwh2 gallus gall
29	289	15.4	581	1 FR12_DROME	P18537 drosophila
30	287.5	15.3	523	1 FZD2_CHICK	Q9ia06 gallus gall
31	285.5	15.2	586	1 FZD4_XENLA	Q9deb5 xenopus lae
32	282	15.0	581	1 FZ10_HUMAN	Q9ulw2 homo sapien
33	271.5	14.4	523	1 FZD4_XENLA	Q9r622 xenopus lae

ALIGNMENTS

RESULT 1

ID	FRZB_BOVIN	STANDARD;	PRT;	325 AA.
AC	Q95117;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Frizzled-related protein precursor (Frzb-1).			
GN	FRZB OR FRZB1.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cartilage;			
RX	MEDLINE=96421609; PubMed=8824257;			
RA	Hoang B., Moos M. Jr., Vukicevic S., Luyten F.P.;			
RT	"Primary structure and tissue distribution of FRZB, a novel protein related to Drosophila frizzled, suggest a role in skeletal morphogenesis."			
RT	J. Biol. Chem. 271:26131-26137(1996).			
RN	[2]			
RP	INTERACTION BETWEEN THE FZ DOMAIN AND WNT PROTEINS.			
RX	MEDLINE=97470942; PubMed=9326585;			
RA	Lin K., Wang S., Julius M.A., Kitajewski J., Moos M. Jr., Luyten F.P.;			
RT	"The cysteine-rich frizzled domain of Frzb-1 is required and sufficient for modulation of Wnt signaling."			
RT	Proc. Natl. Acad. Sci. U.S.A. 94:11198-11200(1997).			
CC	-!- FUNCTION: MAY BE INVOLVED IN MORPHOGENESIS OF SKELETON. MAY ALSO ACT AS A SOLUBLE WNT-BINDING PROTEIN THAT MAY ANTAGONIZE WNT SIGNALING.			
CC	-!- SUBCELLULAR LOCATION: Secreted (Probable).			
CC	-!- DOMAIN: The FZ domain is involved in binding with Wnt ligands.			
CC	-!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.			
CC	-!- SIMILARITY: CONTAINS 1 NTR DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; U24164; AAC48662.1; ..			
DR	InterPro; IPR000024; Fz_domain.			
DR	InterPro; IPR001134; Netrin_C.			
DR	Pfam; PF01392; Fz; 1.			
DR	Pfam; PF01759; NTR; 1.			
DR	SMART; SM00063; FRL; 1.			
DR	PROSITE; PS50038; FZ; 1.			
KW	Glycoprotein; Signal.			
FT	SIGNAL 1 32			POTENTIAL.
FT	CHAIN 33 325			FRIZZLED-RELATED PROTEIN.

34	265	14.1	537	1 FZD4_HUMAN	Q9ulv1 homo sapien
35	263.5	14.0	666	1 FZD3_MOUSE	Q61086 mus musculus
36	262.5	14.0	664	1 FZD3_XENLA	Q42579 xenopus lae
37	262.5	14.0	666	1 FZD3_HUMAN	Q9npg1 homo sapien
38	260	13.8	525	1 FZD4_CHICK	Q9ia05 gallus gall
39	259	13.8	538	1 FZD4_RAT	Q9qzh0 rattus norv
40	255	13.6	537	1 FZD4_MOUSE	Q61088 mus musculus
41	228	12.1	705	1 FR24_DROME	Q9nbw1 drosophila
42	220	11.7	706	1 FZD6_HUMAN	O60353 homo sapien
43	215.5	11.5	709	1 FZD6_MOUSE	Q61089 mus musculus
44	215	11.4	1042	1 COR1_HUMAN	Q9y5q5 homo sapien
45	204	10.9	1113	1 COR1_MOUSE	Q9z319 mus musculus

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FT DOMAIN 33 150 FZ.
FT SITE 165 294 SER-RICH.
FT CARBOHYD 301 318 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 325 AA; 36234 MW; 39E337A9C6E98BB3 CRC64;

Query Match 44.2%; Score 831; DB 1; Length 325;
Best Local Similarity 51.4%; Pred. No. 3.1e-62;
Matches 166; Conservative 48; Mismatches 77; Indels 32; Gaps 8;

QY 3 LSIIVLALCLWLHLAGVRGAPCEAVRIPMCRHMPWNTTRPNHLHSHSTQNAIILAIOYE 62
DB 16 LLVLAALCL-LRVP-GAARAAACEPVRIPLCKSLPNNMTKMPNHLHSHSTQNAIILAIOQE 73
QY 63 ELVDVNCNSAVLRFFECAMYPICITLFLHDPITKPKSCVQCORADDCCEPLMKMYHNSWPES 122
DB 74 GLIGTHCSPDLLFLCLMAYAPICTIDFQHEPIKPKSCVCRAROCCEPILIKYHNSWPES 133
QY 123 LACDELPHYDRGVCISPEAIVT-----DLPEVKWIDITPDMVQERPLDVKRSLSPDRC 178
DB 134 LACELPVYDRGVCISPEAIVTADGAPMDSS-----NGNCRGASSERC 178
QY 179 KCKVKPTLATYLSKNYSYVIHAKIVQSGCNEVTVDVVKRIFKSS-SPIPTQVPL 237
DB 179 KCKPVTRATQRTYFNRYNYIRAKVKEI-KTKCHDVTAVVEKILKASLVNIPRETVNL 237
QY 238 ITNSSCCPHILPHODVLINCY--EWSRMMLLENCIVKWDOLSKRSIOWEERLEOR 295
DB 238 YTSGCCLPPLVNNVEYLNGYDEERSRLVLLVEGSAERKWKDLGRKVRWDMKLRHLG 297
QY 296 RTVOD-----KKKTAGRTSRS 311
DB 298 LNTSDSSHSSTQSKPGRNSNS 320

RESULT 2
ID FRZB_MOUSE STANDARD; PRT; 323 AA.
AC P97401; 009075; 009093;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE -15-JUN-2002 (Rel. 41, Last annotation update)
DE Frizzled-related protein precursor (Frzb-1) (Frizzled) (Fritz)
DE (Secreted frizzled-related sequence protein 3) (sFRP-3).
GN FRZB OR FRZB1 OR FRE OR SFRP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97236495; PubMed=9118218;
RA Leyns L., Bouwmeester T., Kim S.H., Piccolo S., De Robertis E.M.;
RT "Frzb-1 is a secreted antagonist of Wnt signaling expressed in the
RT Spemann organizer.";
RL Cell 88:747-756(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97250455; PubMed=9096311;
RA Ratner A., Hsieh J.C., Smallwood P.M., Gilbert D.J., Copeland N.G.,
RA Jenkins N.A., Nathans J.;
RT "A family of secreted proteins contains homology to the cysteine-rich
RT ligand-binding domain of frizzled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:2859-2863(1997).
RN [4]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wyszaw-Borls A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- FUNCTION: MAY BE INVOLVED IN MORPHOGENESIS OF SKELETON. MAY ALSO
CC ACT AS A SOLUBLE WNT-BINDING PROTEIN THAT MAY ANTAGONIZE WNT
CC SIGNALING.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- DOMAIN: The FZ domain is involved in binding with Wnt ligands (By
CC similarity).
CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 NTR DOMAIN.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U68058; AAC53135.1; -
CC EMBL: U91905; AAB51300.1; -
CC EMBL: U88568; AAC53147.1; -
CC EMBL: AK019093; BAB31542.1; -
CC MGD: MGI:892032; Frzb.
CC InterPro: IPR000024; Fz_domain.
CC InterPro: IPR001134; Netrin_C.
CC Pfam: PF01392; Fz; 1.
CC Pfam: PF01759; NTR; 1.
CC SMART: SM00063; FRI; 1.
CC PROSITE: PS50038; FZ; 1.
CC Glycoprotein; Signal.
KW SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 323 FRIZZLED-RELATED PROTEIN.
FT DOMAIN 33 150 FZ.
FT DOMAIN 165 294 NTR.
FT SITE 301 318 SER/THR-RICH.
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 323 AA; 36011 MW; 3F1456F8CF97740 CRC64;

Query Match 44.2%; Score 830; DB 1; Length 323;
Best Local Similarity 50.8%; Pred. No. 3.7e-62;
Matches 166; Conservative 50; Mismatches 77; Indels 34; Gaps 9;

QY 3 LSIIVLALCLWLHLAGVRGAPCEAVRIPMCRHMPWNTTRPNHLHSHSTQNAIILAIOYE 62
DB 16 LLVLAALCL-LQVP-GAARAAACEPVRIPLCKSLPNNMTKMPNHLHSHSTQNAIILAIOQE 73
QY 63 ELVDVNCNSAVLRFFECAMYPICITLFLHDPITKPKSCVQCORADDCCEPLMKMYHNSWPES 122
DB 74 GLIGTHCSPDLLFLCLMAYAPICTIDFQHEPIKPKSCVCRAROCCEPILIKYHNSWPES 133
QY 123 LACDELPHYDRGVCISPEAIVT-----DLPEVKWIDITPDMVQERPLDVKRSLSPDRC 178

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Db 134 LACDELVDYDGVGVCISPEAIVTAGDADFPMDS-----TCHCRGASSERC 178
QY 179 KCKVPTATLTKYVYVIAKAVORSGNEVTTVVDVKEIFKSS-SPIPRTOVPL 237
Db 179 KCPVATQKTYFRNNYVIRAKVEKMK-CHDVAVVEVEKEILKSLVNPRTVNL 237
QY 238 ITNSSCQCCHILPHODVLINCY--EWSRMMLLENCLVEKWRDOLSKRSIQWERLQ--- 292
Db 238 YTTSGCLCPPLTNEEVINGYEDEERSRLLVGEGSIAEKWKDRLGKVKRWDMKLRHLG 297
QY 293 -----EQRRTVQDKKTKAGTNRSPK 315
Db 298 LGKTDASDSTQNK--SGRNSRPPAR 322
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RESULT 3

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FRZB_HUMAN STANDARD; PRT; 325 AA.
ID FRZB_HUMAN Q92765; O00181; Q99686;
AC Q92765; O00181; Q99686;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Frizzled-related protein precursor (Frzb-1) (Frizzled) (Fritz).
GN FRZB OR FRZB1 OR FRE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96421609; PubMed=8824257;
RA Hoang B., Moos M. Jr., Yukevic S., Luyten F.P.;
RT "Primary structure and tissue distribution of FRZB, a novel protein related to Drosophila frizzled, suggest a role in skeletal morphogenesis.";
RL J. Biol. Chem. 271:26131-26137(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Mayr T., Deutsch U., Kuehl M., Drexler H.C.A., Lottspeich F.,
RA Deutmann R., Wedlich D., Risau W.;
RT "Fritz: a secreted frizzled-related protein that inhibits Wnt activity.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=97236495; PubMed=9118218;
RA Leyns L., Boumeester T., Kim S.-H., Piccolo S., de Robertis E.M.;
RT "Frzb-1 is a secreted antagonist of Wnt signaling expressed in the Spemann organizer.";
RL Cell 88:747-756(1997).
CC -!- FUNCTION: MAY BE INVOLVED IN MORPHOGENESIS OF SKELETON. MAY ALSO ACT AS A SOLUBLE WNT-BINDING PROTEIN THAT MAY ANTAGONIZE WNT SIGNALING.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THE CARTILAGINOUS CORES OF THE LONG BONE DURING EMBRYONIC AND FETAL DEVELOPMENT AND IN THE APPENDICULAR SKELETON (6-13 WEEKS). AT 13 WEEKS OF GESTATION, TRANSCRIPTS WERE PRESENT IN EARLY CHONDROBLASTS OF THE TARSAL BONES OF THE FOOT, THE CARPAL BONES OF THE HANDS AND THE EPIPHYSIS OF LONG BONES. HIGHLY EXPRESSED IN PLACENTA AND HEART. FOLLOWED BY BRAIN, SKELETAL MUSCLE, KIDNEY AND PANCREAS. WEAKLY EXPRESSED IN LUNG AND LIVER.
CC -!- DOMAIN: The Fz domain is involved in binding with Wnt ligands (By similarity).
CC -!- SIMILARITY: CONTAINS 1 FRIZZLED (Fz) DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 NTR DOMAIN.
CC -----
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CC -----
CC EMBL: U24163; AAC50736.1; -.
DR EMBL: U91903; AAB51298.1; -.
DR EMBL: U68057; AAC51217.1; -.
DR Genew: HGNC:3959; FRZB.
DR MIM: 605083; -.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR001134; Netrin_C.
DR Pfam: PF01392; Fz; 1.
DR Pfam: PF01759; NTR; 1.
DR SMART: SM00063; FRI; 1.
DR PROSITE: PS00038; FZ; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 32
FT CHAIN 33 325
FT DOMAIN 33 150
FT DOMAIN 165 294
FT SITE 301 318
FT CARBOHYD 49 49
FT CONFLICT 63 63 A -> D (IN REF. 2).
FT CONFLICT 106 106 K -> N (IN REF. 1).
SQ SEQUENCE 325 AA; 36254 MW; 8337C51BBA9A4B07 CRC64;

Query Match 44.1%; Score 828; DB 1; Length 325;
Best Local Similarity 50.8%; Pred. No. 5.4e-62;
Matches 164; Conservative 51; Mismatches 78; Indels 30; Gaps 8;

QY 3 LSTLVALCLWLHLALGVGAPCAVRIPMCRHMPWNTTRMPNHLHSTOENALIAEYOE 62
Db 16 LLALALCL-LRVP-GARAAACEPVRIPLCKSLPWNTRMPNHLHSTQNALIAEQFE 73
QY 63 ELVDVNCASVAVRFFFCAMYPACTLEFLHDPIPKCSVCORADDCPEPLMKMYNHSWPE 122
Db 74 GLLGTHCSPDLLFFLCAMYPACTIDFQHEPIPKCSVCERAROGCEPILIKYRHSWPN 133
QY 123 MACDELVDYDGVGVCISPEAIVT-----DLPEVKWIDITPDMVQERPLDVKRLSPDRC 178
Db 134 LACEELVDYDGVGVCISPEAIVTAGDADFPMDS-----NCGRGASSERC 178
QY 179 KCKVPTATLTKYVYVIAKAVORSGNEVTTVVDVKEIFKSS-SPIPRTOVPL 237
Db 179 KCPVATQKTYFRNNYVIRAKVEI-KTKCHDVAVVEVEKEILKSLVNPRTVNL 237
QY 238 ITNSSCQCCHILPHODVLINCY--EWSRMMLLENCLVEKWRDOLSKRSIQWERLQEQR 295
Db 238 YTTSGCLCPPLNVEEVIINGYEDEERSRLLVGEGSIAEKWKDRLGKVKRWDMKLRHLG 297
QY 296 RTVQDKKTKAGTNR-----SNP 313
Db 298 LSKSDSNSTQSTQSKSGRNSNP 320

RESULT 4
FRZ5_HUMAN STANDARD; PRT; 585 AA.
ID FRZ5_HUMAN Q13467;
AC Q13467;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Frizzled 5 precursor (Frizzled-5) (Fz5) (FzE5).
GN FZD5 OR HFZ5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=96224032; PubMed=8626800;
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RA Wang Y., Macke J.P., Abella B.S., Andreasson K., Worley P.,
RA Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;
RT "A large family of putative transmembrane receptors homologous to the
RL product of the *Drosophila* tissue polarity gene *frizzled*.";
RN J. Biol. Chem. 271:4468-4476(1996).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21301556; PubMed=11408929;
RA Saitoh T., Hirai M., Katoh M.;
RT "Molecular cloning and characterization of human *Frizzled-5* gene on
RT chromosome 2q33.3-q34 region.";
RN Int. J. Oncol. 19:105-110(2001).
[3]
RP SEQUENCE OF 273-331 FROM N.A.
RX TISSUE-Oesophageal carcinoma;
RA MEDLINE=98374323; PubMed=9707618;
RA Tanaka S., Akiyoshi T., Mori M., Wands J.R., Sugimachi K.;
RT "A novel frizzled gene identified in human esophageal carcinoma
RT mediates APC/beta-catenin signals.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:10164-10169(1998).
[4]
RP COUPLING TO BETA-CATENIN PATHWAY.
RX MEDLINE=97207341; PubMed=9054360;
RA He X., Saint-Jeanet J.P., Wang Y., Nathans J., Dawid I., Varmus H.;
RT "A member of the Frizzled protein family mediating axis induction by
RT Wnt-5A.";
RL Science 275:1652-1654(1997).
CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
CC are coupled to the beta-catenin canonical signaling pathway, which
CC leads to the activation of dishevelled proteins, inhibition of
CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
CC of Wnt target genes. A second signaling pathway involving PKC and
CC calcium fluxes has been seen for some family members, but it is
CC not yet clear if it represents a distinct pathway or if it can be
CC integrated in the canonical pathway, as PKC seems to be required
CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
CC to involve interactions with G-proteins. May be involved in
CC transduction and intercellular transmission of polarity
CC information during tissue morphogenesis and/or in differentiated
CC tissues. Interacts specifically with Wnt5A to induce the beta-
CC catenin pathway.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DOMAIN: Lys-Thr-X-X-TRP motif is involved in the activation of
CC the Wnt/beta-catenin signaling pathway (By similarity).
CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SNO OF G-PROTEIN COUPLED
CC RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: UA3318; AAC50385.1; -;
CC EMBL: AB043702; BAB60959.1; -;
CC Genbank: HGNC:4043; FZD5.
CC MIM: 601723; -;
CC InterPro: IPR000539; Frizzled.
CC InterPro: IPR000024; Fz_domain.
CC InterPro: IPR000832; GPCR_secretin.
CC Pfam: PF01392; Fz; 1.
CC Pfam: PF01534; Frizzled; 1.
CC PRINTS: PR00489; FRIZZLED.
CC SMART: SM00063; FRI; 1.
CC PROSITE: PS50038; FZ; 1.
CC PROSITE: PS50261; G-PROTEIN_RECEP_F2_4; 1.
KW Multigene family; G-protein coupled receptor; Transmembrane;
KW Developmental protein; Glycoprotein; Signal.

FT SIGNAL 1 26
FT CHAIN 27 585
FT DOMAIN 27 238
FT TRANSMEM 239 259
FT DOMAIN 260 270
FT TRANSMEM 271 291
FT DOMAIN 292 315
FT TRANSMEM 316 336
FT DOMAIN 337 358
FT TRANSMEM 359 379
FT DOMAIN 380 402
FT TRANSMEM 403 423
FT DOMAIN 424 449
FT TRANSMEM 450 470
FT DOMAIN 471 500
FT TRANSMEM 501 521
FT DOMAIN 522 585
FT DOMAIN 28 150
FT SITE 525 530
FT SITE 583 585
FT CARBOHYD 47 47
FT CARBOHYD 151 151
FT CONFLICT 88 88
FT CONFLICT 262 263
FT CONFLICT 345 345
FT CONFLICT 357 357
FT CONFLICT 402 402
SQ SEQUENCE 585 AA; 64551 MW; CF66C5BA746E7971 CRC64;

Query Match 18.0%; Score 338.5; DB 1; Length 585;
Best Local Similarity 33.3%; Pred. No. 8.4e-21;
Matches 73; Conservative 37; Mismatches 84; Indels 25; Gaps 6;

QY 5 ILVALCLMLHALGVRCAP-CEAVRIPMCRHMPNITRMPNHLHSHSTQENAILAEQVEE 63
Db 13 LLLLAQLVGRAAASKAPVCQEITVPMCRGIGYNLTHMPNQFNHDITQDCAGLEVHQFWP 72
QY 64 LVDVNCSAVLRFFFCAMYPACTLEFLHDPKCKSYCORARDCEPLMKMNHNSWPESL 123
Db 73 LVEIQCSPLDRFFLCITWTPTICLPDY-HKPLPPCRSVCRKAGCSPLMRQYGFAMPERM 131
QY 124 ACDELPPYDRGVCLISPEAIVTDLPEDVKWIDITPDMVMQVERPL-----DVDCKRL 173
Db 132 SCDRPLPLVGR-----DAEVLCDMDYNRSEATTAPRPPFAKPTLPGPPGASGECGAC 185
QY 174 SPDRCKCKK-VKPTLATYLSKNYSYVTHAKIKAVQSGC 211
Db 186 GPFCVKCRPEFVPL-----KESHPDYNKVRVGQVPNC 218

RESULT 5
FZD5_MOUSE
ID FZD5_MOUSE STANDARD; PRT; 577 AA.
AC Q9EQD0; O08975;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Frizzled 5 precursor (Frizzled-5) (Fz-5) (mFz5).
GN FZD5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6N; TISSUE=Gut;
RX PubMed=11092808;
RA Ishikawa T., Tamai Y., Zorn A.M., Yoshida H., Seldin M.F.,
RA Nishikawa S.-I., Taketo M.M.;
RT "Mouse Wnt receptor gene *Fzd5* is essential for yolk sac and placental
RT angiogenesis";
RN Development 128:25-33(2001).
RN [2]

SEQUENCE OF 207-296 FROM N.A.
SPRAIN-C57BL/6; TISSUE=Prostate;
Johnson M.A., Greenberg N.M.;
Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
[3]
TISSUE SPECIFICITY
MEDLINE=96224032; PubMed=8626800;
Wang Y., Macke J.P., Abella B.S., Andreasson K., Worley P.,
Johnson M.A., Copeland N.G., Jenkins N.A., Nathans J.;
"A large family of putative transmembrane receptors homologous to the
product of the Drosophila tissue polarity gene frizzled.";
J. Biol. Chem. 271:4468-4476(1996).
- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
are coupled to the beta-catenin canonical signaling pathway, which
leads to the activation of dishevelled proteins, inhibition of
GSK-3 kinase, nuclear accumulation of beta-catenin and activation
of Wnt target genes. A second signaling pathway involving PKC and
calcium fluxes has been seen for some family members, but it is
not yet clear if it represents a distinct pathway or if it can be
integrated in the canonical pathway, as PKC seems to be required
for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
to involve interactions with G-proteins. May be involved in
transduction and intercellular transmission of polarity
information during tissue morphogenesis and/or in differentiated
tissues. Plays a role in yolk sac angiogenesis and in placental
vascularization. Binds to Wnt2, Wnt10B, Wnt5A, but not to Wnt2B or
Wnt4.
- SUBCELLULAR LOCATION: Integral membrane protein.
- TISSUE SPECIFICITY: Expressed in eye, kidney, lung, chondrocytes,
epithelial cells of the small intestine and goblet cells of the
colon.
- DEVELOPMENTAL STAGE: Expressed in the yolk sac, placenta, eye and
lung bud at 9.5 days post coitum (dpc). At 10.5 dpc, also
expressed in the placental blood vessel of embryonic origin.
- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
similarity).
- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
RECEPTORS.
- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

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EMBL; AF272146; AAC39355.1; -
EMBL; AF005203; AAC01953.1; -
MGD; MGI:108571; Fzd5.
InterPro: IPR000539; Frizzled.
InterPro: IPR000024; Fz_domain.
DR InterPro: IPR000832; GPCR_secretin.
Pfam; PF01392; Fz; 1.
Pfam; PF01534; Frizzled; 2.
PRINTS; PR00489; FRIZZLED.
SMART; SM00063; FRI; 1.
PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50261; G-PROTEIN_RECPT_F2_4; 1.
KW Multigene family; G-protein coupled receptor; Transmembrane;
KW Developmental protein; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 577
FT DOMAIN 27 234
FT TRANSMEM 235 255
FT DOMAIN 256 267
FT TRANSMEM 267 286
FT DOMAIN 288 311
FT TRANSMEM 312 332
FT DOMAIN 333 354
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FT DOMAIN 3649 3668
FT TRANSMEM 3668 3687
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FT TRANSMEM 3706 3725
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FT DOMAIN 3763 3782
FT TRANSMEM 3782 3801
FT DOMAIN 3801 3820
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FT DOMAIN 3953 3972
FT TRANSMEM 3972 3991
FT DOMAIN 3991 4010
FT TRANSMEM 4010 4029
FT DOMAIN 4029 4048
FT TRANSMEM 4048 4067
FT DOMAIN 4067 4086
FT TRANSMEM 4086 4105
FT DOMAIN 4105

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasaman D.A., Welstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
CC are coupled to the beta-catenin canonical signaling pathway, which
CC leads to the activation of dishevelled proteins. Inhibition of
CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
CC of Wnt target genes. A second signaling pathway involving PKC and
CC calcium fluxes has been seen for some family members, but it is
CC not yet clear if it represents a distinct pathway or if it can be
CC integrated in the canonical pathway, as PKC seems to be required
CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
CC to involve interactions with G-proteins. Required to coordinate
CC the cytoskeletons of epidermal cells to produce a parallel array
CC of cuticular hairs and bristles.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- DEVELOPMENTAL STAGE: Expression starts at stage 6 in all cells
CC between 15 and 70 per cent of egg length, including the
CC invaginating cells of the ventral furrow. Stripe pattern is
CC emerging by early stage 8. From stage 9 and continuing throughout
CC embryogenesis, expression is seen in the developing CNS. At stage
CC 10, expressed in 15 stripes in the presumptive head and trunk
CC regions, in the posterior midgut primordium, in a subset of cells
CC of anterior midgut invagination and in the procephalic lobe. At
CC stage 12, expression declines in epidermis and increases in the
CC midgut and visceral mesoderm. At stage 17, only expressed in the
CC CNS, hindgut and dorsal vessel.
CC -1- DOMAIN: Lys-Thr-x-x-Trp motif is involved in the activation of
CC the Wnt/beta-catenin signaling pathway (By similarity).
CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands.
CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
CC RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
CC -----
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CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL: U65589; AAC47273.1; -;
DR EMBL: AE003518; AAF49184.1; -;
DR FlyBase: FBgn0016797; fz2.
DR InterPro: IPR000539; Frizzled.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR000832; GPCR_secretin.
DR Pfam: PF01534; Frizzled; 1.
DR Pfam: PF01392; Fz; 1.
DR PRINTS: PR00489; FRIZZLED.
DR SMART: SM00063; FRI; 1.
DR PROSITE: PS50038; FZ; 1.
DR PROSITE: PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Multigene family; Receptor; G-protein coupled receptor; Transmembrane;
KW Developmental protein; Glycoprotein; Signal.

FT	SIGNAL	1	22	POTENTIAL.
FT CHAIN	23	694		FRIZZLED PROTEIN 2.
FT DOMAIN	23	315		EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	316	336		1 (POTENTIAL).
FT DOMAIN	337	352		CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	353	373		2 (POTENTIAL).
FT DOMAIN	374	397		EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	398	418		3 (POTENTIAL).
FT DOMAIN	419	439		CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	440	460		4 (POTENTIAL).
FT DOMAIN	461	482		EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	483	503		5 (POTENTIAL).
FT DOMAIN	504	534		CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	535	555		6 (POTENTIAL).
FT DOMAIN	556	584		EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	585	605		7 (POTENTIAL).
FT DOMAIN	606	694		CYTOPLASMIC (POTENTIAL).
FT DOMAIN	187	225		GLY-RICH.
FT SITE	608	613		FZ.
FT SITE	692	694		LYS-THR-X-X-TRP MOTIF.
FT CARBOHYD	78	78		PO2-BINDING.
FT CARBOHYD	288	288		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT	55	55		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT	417	417		V -> A (IN REF. 1).
FT CONFLICT	417	417		S -> T (IN REF. 1).
SQ	SEQUENCE	694 AA; 75451 MW;	6C510F13CBFAFB096 CRC64;	

Query Match 16.9%; Score 318; DB 1; Length 694;
Best Local Similarity 39.4%; Pred. No. 5.4e-19;
Matches 56; Conservative 25; Mismatches 37; Indels 24; Gaps 2;

QY	24	CEAVRIPMCRHMPWNTITRMPNHLHSTQENAILAIEQYELVDVNCNSAVLRFFFCAMYP	83'
Db	64	CEITIPMCRGICYNMTSPFNENHETQDEAGLEWFLVEIKCSPDLKFLCSMYTP	123
QY	84	ICTLEFLHDPKCKSVQCRARDCEPLMKYHNHWPESLACDELPPYDVRGVCISPAIV	143
Db	124	IC-LEDYHKPLPVCRSVCRARSCAPIMQOYSFEPWERMACEHLPLHG	171
QY	144	TDLPEDVKWIDITPDMMVOERP	165
Db	172	-----DPDNLCMEQP	181

RESULT 7
FZD9_HUMAN STANDARD; PRT; 591 AA.
ID FZD9_HUMAN
AC Q00144;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Frizzled 9 precursor (Frizzled-9) (Fz-9) (hFz9) (FzE6).
GN FZD9 OR FZD9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=9727293; PubMed=9147651;
RA Wang Y.-K., Samos H.C., Peoples R., Perez-Jurado L.A., Nusse R.,
RA Francke U.;
RT "A novel human homologue of the *Drosophila* frizzled wnt receptor gene
RT binds wingless protein and is in the Williams syndrome deletion at
RT 7q11.23.";
RL Hum. Mol. Genet. 6:465-472(1997).
RN [2]
RP SEQUENCE OF 269-329 FROM N.A.
RC TISSUE=Oesophageal carcinoma.
RX MEDLINE=98374323; PubMed=9707618;
RA Tanaka S., Akiyoshi T., Mori M., Wands J.R., Sugimachi K.;
RT "A novel frizzled gene identified in human esophageal carcinoma

RA Calo L., Mimmack M.L., Keverne E.B., Emson P.C.;
 RT "Localization of the mouse frizzled gene mFzd3 in the olfactory
 RL epithelium and in the vomeronasal organ.";
 CC Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 CC are coupled to the beta-catenin canonical signaling pathway, which
 CC leads to the activation of dishevelled proteins, inhibition of
 CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 CC of Wnt target genes. A second signaling pathway involving PKC and
 CC calcium fluxes has been seen for some family members, but it is
 CC not yet clear if it represents a distinct pathway or if it can be
 CC integrated in the canonical pathway, as PKC seems to be required
 CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 CC to involve interactions with G-proteins. May be involved in
 CC transduction and intercellular transmission of polarity
 CC information during tissue morphogenesis and/or in differentiated
 CC tissues.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Localizes in the
 CC plasma membrane.
 CC -!- TISSUE SPECIFICITY: In the embryo, found in the neural tube, trunk
 CC skeletal muscle precursors (myotomes), limb skeletal anlagen,
 CC craniofacial regions and nephric ducts. In the adult, expression
 CC is abundant in heart, brain, testis and skeletal muscle. In the
 CC testis, expressed in all spermatogenic cell types. Lower levels in
 CC adult lung, liver and kidney. Barely detectable in spleen.
 CC Expressed also in chondrocytes.
 CC -!- DEVELOPMENTAL STAGE: Not detected at embryonic day 7 (E7), weakly
 CC at E11 and strongly at E15 and E17. Expression covers the entire
 CC neural tube at day 9.5 post-coitum (dpc), decreases at 10.5 dpc
 CC and becomes detectable only in the lumbar to tail regions at 11.5
 CC dpc. In the somites, expression begins at 10.5 dpc to become
 CC upregulated all along the rostrocaudal trunk axis at 11.5 dpc. In
 CC craniofacial territories, expression is first detected at 11.5 dpc
 CC in restricted areas of the nose, the maxillary mandibular and
 CC second branchial arch anlagen. At 11.5 dpc, predominantly
 CC expressed in restricted areas of the nose, dorsally to the eye and
 CC in the caudal pharyngeal region.
 CC -!- DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of
 CC the Wnt/beta-catenin signaling pathway (By similarity).
 CC -!- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
 CC similarity).
 CC -!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC -!- SIMILARITY: CONTAINS 1 FRIZZLED (Fz) DOMAIN.
 CC -!- CAUTION: Has been first described as Fzd3 in litterature.
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 CC -----
 CC EMBL: AF088850; AAD27789.1; -;
 CC DR EMBL: AK021164; BAB32311.1; -;
 CC DR EMBL: AF033585; AAB87503.2; -;
 CC DR EMBL: Y17709; CAB44237.1; -;
 CC DR MGD: MGI:1313278; Fzd9.
 CC DR InterPro: IPR000539; Frizzled.
 CC DR InterPro: IPR000024; Fz_domain.
 CC DR InterPro: IPR01392; Fz; 2.
 CC DR Pfam: PF01534; Frizzled; 3.
 CC DR PRINTS: PR00489; *FRIZZLED.
 CC DR SMART: SM00063; Fw1; 1.
 CC DR PROSITE: PS50038; Fz; 1.
 CC DR PROSITE: PS50261; G_PROTEIN_RECEP_F2_4; 1.
 CC KW Multigene family; G-protein coupled receptor; Transmembrane;
 CC KW developmental protein; Glycoprotein; Signal.
 CC FT SIGNAL 1 23 POTENTIAL.
 CC FT CHAIN 24 592 FRIZZLED 9.
 CC FT DOMAIN 24 230 EXTRACELLULAR.

FT TRANSMEM 231 251 1 (POTENTIAL).
 FT DOMAIN 252 267 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 268 288 2 (POTENTIAL).
 FT DOMAIN 289 316 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 317 337 3 (POTENTIAL).
 FT DOMAIN 338 356 CYTOPLASMIC (POTENTIAL).
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 FT TRANSMEM 510 530 9 (POTENTIAL).
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 FT DOMAIN 593 615 11 (POTENTIAL).
 FT SITE 616 638 12 (POTENTIAL).
 FT CARBOHYD 639 659 13 (POTENTIAL).
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 FT CONFLICT 681 701 15 (POTENTIAL).
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 FT CONFLICT 5592 5612 249 (POTENTIAL).
 FT CONFLICT 5613 5633 250 (POTENTIAL).
 FT CONFLICT 5634 5654 251 (POTENTIAL).
 FT CONFLICT 5655 5675 252 (POTENTIAL).
 FT CONFLICT 5676 5696 253 (POTENTIAL).
 FT CONFLICT 5697 5717 254 (POTENTIAL).
 FT CONFLICT 5718 5738 255 (POTENTIAL).
 FT CONFLICT 5739 5759 256 (POTENTIAL).
 FT CONFLICT 5760 5780 257 (POTENTIAL).
 FT CONFLICT 5781 5801 258 (POTENTIAL).
 FT CONFLICT 5802 5822 259 (POTENTIAL).
 FT CONFLICT 5823 5843 260 (POTENTIAL).
 FT CONFLICT 5844 5864 261 (POTENTIAL).
 FT CONFLICT 5865 5885 262 (POTENTIAL).
 FT CONFLICT 5886 5906 263 (POTENTIAL).
 FT CONFLICT 5907 5927 264 (POTENTIAL).
 FT CONFLICT 5928 5948 265 (POTENTIAL).
 FT CONFLICT 5949 5969 266 (POTENTIAL).
 FT CONFLICT 5970 5990 267 (POTENTIAL).
 FT CONFLICT 5991 6011 268 (POTENTIAL).
 FT CONFLICT 6012 6032 269 (POTENTIAL).
 FT CONFLICT 6033 6053 270 (POTENTIAL).
 FT CONFLICT 6054 6074 271 (POTENTIAL).
 FT CONFLICT 6075 6095 272 (POTENTIAL).
 FT CONFLICT 6096 6116 273 (POTENTIAL).
 FT CONFLICT 6117 6137 274 (POTENTIAL).
 FT CONFLICT 6138 6158 275 (POTENTIAL).
 FT CONFLICT 6159 6179 276 (POTENTIAL).
 FT CONFLICT 6180 6200 277 (POTENTIAL).
 FT CONFLICT 6201 6221 278 (POTENTIAL).
 FT CONFLICT 6222 6242 279 (POTENTIAL).
 FT CONFLICT 6243 6263 280 (POTENTIAL).
 FT CONFLICT 6264 6284 281 (POTENTIAL).
 FT CONFLICT 6285 6305 282 (POTENTIAL).
 FT CONFLICT 6306 6326 283 (POTENTIAL).
 FT CONFLICT 6327 6347 284 (POTENTIAL).
 FT CONFLICT 6348 6368 285 (POTENTIAL).
 FT CONFLICT 6369 6389 286 (POTENTIAL).
 FT CONFLICT 6390 6410 287 (POTENTIAL).
 FT CONFLICT 6411 6431 288 (POTENTIAL).
 FT CONFLICT 6432 6452 289 (POTENTIAL).
 FT CONFLICT 6453 6473 290 (POTENTIAL).
 FT CONFLICT 6474 6494 291 (POTENTIAL).
 FT CONFLICT 6495 6515 292 (POTENTIAL).
 FT CONFLICT 6516 6536 293 (POTENTIAL).
 FT CONFLICT 6537 6557 294 (POTENTIAL).
 FT CONFLICT 6558 6578 295 (POTENTIAL).
 FT CONFLICT 6579 6599 296 (POTENTIAL).
 FT CONFLICT 6600 6620 297 (POTENTIAL).
 FT CONFLICT 6621 6641 298 (POTENTIAL).
 FT CONFLICT 6642 6662 299 (POTENTIAL).
 FT CONFLICT 6663 6683 300 (POTENTIAL).
 FT CONFLICT 6684 6704 301 (POTENTIAL).
 FT CONFLICT 6705 6725 302 (POTENTIAL).
 FT CONFLICT 6726 6746 303 (POTENTIAL).
 FT CONFLICT 6747 6767 304 (POTENTIAL).
 FT CONFLICT 6768 6788 305 (POTENTIAL).
 FT CONFLICT 6789 6809 306 (POTENTIAL).
 FT CONFLICT 6810 6830 307 (POTENTIAL).
 FT CONFLICT 6831 6851 308 (POTENTIAL).
 FT CONFLICT 6852 6872 309 (POTENTIAL).
 FT CONFLICT 6873 6893 310 (POTENTIAL).
 FT CONFLICT 6894 6914 311 (POTENTIAL).
 FT CONFLICT 6915 6935 312 (POTENTIAL).
 FT CONFLICT 6936 6956 313 (POTENTIAL).
 FT CONFLICT 6957 6977 314 (POTENTIAL).
 FT CONFLICT 6978 6998 315 (POTENTIAL).
 FT CONFLICT 6999 7019 316 (POTENTIAL).
 FT CONFLICT 7020 7040 317 (POTENTIAL).
 FT CONFLICT 7041 7061 318 (POTENTIAL).
 FT CONFLICT 7062 7082 319 (POTENTIAL).
 FT CONFLICT 7083 7103 320 (POTENTIAL).
 FT CONFLICT 7104 7124 321 (POTENTIAL).
 FT CONFLICT 7125 7145 322 (POTENTIAL).
 FT CONFLICT 7146 7166 323 (POTENTIAL).
 FT CONFLICT 7167 7187 324 (POTENTIAL).
 FT CONFLICT 7188 7208 325 (POTENTIAL).
 FT CONFLICT 7209 7229 326 (POTENTIAL).
 FT CONFLICT 7230 7250 327 (POTENTIAL).
 FT CONFLICT 7251 7271 328 (POTENTIAL).
 FT CONFLICT 7272 7292 329 (POTENTIAL).
 FT CONFLICT 7293 7313 330 (POTENTIAL).
 FT CONFLICT 7314 7334 331 (POTENTIAL).
 FT CONFLICT 7335 7355 332 (POTENTIAL).
 FT CONFLICT 7356 7376 333 (POTENTIAL).
 FT CONFLICT 7377 7397 334 (POTENTIAL).
 FT CONFLICT 7398 7418 335 (POTENTIAL).
 FT CONFLICT 7419 7439 336 (POTENTIAL).
 FT CONFLICT 7440 7460 337 (POTENTIAL).
 FT CONFLICT 7461 7481 338 (POTENTIAL).
 FT CONFLICT 7482 7502 339 (POTENTIAL).
 FT CONFLICT 7503 7523 340 (POTENTIAL).
 FT CONFLICT 7524 7544 341 (POTENTIAL).
 FT CONFLICT 7545 7565 342 (POTENTIAL).
 FT CONFLICT 7566 7586 343 (POTENTIAL).
 FT CONFLICT 7587 7607 344 (POTENTIAL).
 FT CONFLICT 7608 7628 345 (POTENTIAL).
 FT CONFLICT 7629 7649 346 (POTENTIAL).
 FT CONFLICT 7650 7670 347 (POTENTIAL).
 FT CONFLICT 7671 7691 348 (POTENTIAL).
 FT CONFLICT 7692 7712 349 (POTENTIAL).
 FT CONFLICT 7713 7733 350 (POTENTIAL).
 FT CONFLICT 7734 7754 351 (POTENTIAL).
 FT CONFLICT 7755 7775 352 (POTENTIAL).
 FT CONFLICT 7776 7796 353 (POTENTIAL).
 FT CONFLICT 7797 7817 354 (POTENTIAL).
 FT CONFLICT 7818 7838 355 (POTENTIAL).
 FT CONFLICT 7839 7859 356 (POTENTIAL).
 FT CONFLICT 7860 7880 357 (POTENTIAL).
 FT CONFLICT 7881 7901 358 (POTENTIAL).
 FT CONFLICT 7902 7922 359 (POTENTIAL).
 FT CONFLICT 7923 7943 360 (POTENTIAL).
 FT CONFLICT 7944 7964 361 (POTENTIAL).
 FT CONFLICT 7965 7985 362 (POTENTIAL).
 FT CONFLICT 7986 8006 363 (POTENTIAL).
 FT CONFLICT 8007 8027 364 (POTENTIAL).
 FT CONFLICT 8028 8048 365 (POTENTIAL).
 FT CONFLICT 8049 8069 366 (POTENTIAL).
 FT CONFLICT 8070 8090 367 (POTENTIAL).
 FT CONFLICT 8091 8111 368 (POTENTIAL).
 FT CONFLICT 8112 8132 369 (POTENTIAL).
 FT CONFLICT 8133 8153 370 (POTENTIAL).
 FT CONFLICT 8154 8174 371 (POTENTIAL).
 FT CONFLICT 8175 8195 372 (POTENTIAL).
 FT CONFLICT 8196 8216 373 (POTENTIAL).
 FT CONFLICT 8217 8237 374 (POTENTIAL).
 FT CONFLICT 8238 8258 375 (POTENTIAL).
 FT CONFLICT 8259 8279 376 (POTENTIAL).
 FT CONFLICT 8280 8300 377 (POTENTIAL).
 FT CONFLICT 8301 8321 378 (POTENTIAL).
 FT CONFLICT 8322 8342 379 (POTENTIAL).
 FT CONFLICT 8343 8363 380 (POTENTIAL).
 FT CONFLICT 8364 8384 381 (POTENTIAL).
 FT CONFLICT 8385 8405 382 (POTENTIAL).
 FT CONFLICT 8406 8426 383 (POTENTIAL).
 FT CONFLICT 8427 8447 384 (POTENTIAL).
 FT CONFLICT 8448 8468 385 (POTENTIAL).
 FT CONFLICT 8469 8489 386 (POTENTIAL).
 FT CONFLICT 8490 8510 387 (POTENTIAL).
 FT CONFLICT 8511 8531 388 (POTENTIAL).
 FT CONFLICT 8532 8552 389 (POTENTIAL).
 FT CONFLICT 8553 8573 390 (POTENTIAL).
 FT CONFLICT 8574 8594 391 (POTENTIAL).
 FT CONFLICT 8595 8615 392 (POTENTIAL).
 FT CONFLICT 8616 8636 393 (POTENTIAL).
 FT CONFLICT 8637 8657 394 (POTENTIAL).
 FT CONFLICT 8658 8678 395 (POTENTIAL).
 FT CONFLICT 8679 8699 396 (POTENTIAL).
 FT CONFLICT 8700 8720 397 (POTENTIAL).
 FT CONFLICT 8721 8741 398 (POTENTIAL).

*Xenopus frizzled 7 can act in canonical and non-canonical Wnt signaling pathways: implications on early patterning and morphogenesis.";
 Mech. Dev. 92:227-237(2000).
 [3]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=20323171; PubMed=10862746;
 RA Djiane A., Riou J.-F., Umbhauer M., Boucaut J.-C., Shi D.-L.;
 RT "Role of frizzled 7 in the regulation of convergent extension
 movements during gastrulation in Xenopus laevis.";
 RL Development 127:3091-3100(2000).
 [4]
 RN SEQUENCE FROM N.A., AND COUPLING TO BETA-CATENIN PATHWAY.
 RC TISSUE=Oocyte;
 RX MEDLINE=20214855; PubMed=10751186;
 RA Sumanas S., Strege P., Heasman J., Ekker S.C.;
 RT "The putative Wnt receptor Xenopus frizzled-7 functions upstream of
 beta-catenin in vertebrate dorso-ventral mesoderm patterning.";
 RL Development 127:1981-1990(2000).
 [5]
 RN SEQUENCE FROM N.A., AND COUPLING TO BETA-CATENIN PATHWAY.
 RX MEDLINE=20424135; PubMed=10969734;
 RA Brown J.D., Hallagan S.E., McGrew L.L., Miller J.R., Moon R.T.;
 RT "The maternal Xenopus beta-catenin signaling pathway, activated by
 frizzled homologs, induces goosecoid in a cell non-autonomous
 manner.";
 RL Dev. Growth Differ. 42:347-357(2000).
 [6]
 RN SEQUENCE FROM N.A.
 RP Gradi D., Buhrmann V., Wedlich D.;
 RA Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 [7]
 RN COUPLING TO BETA-CATENIN PATHWAY.
 RX MEDLINE=20445927; PubMed=10990458;
 RA Umbhauer M., Djiane A., Golsset C., Penzo-Mendez A., Riou J.-F.,
 Boucaut J.-C., Shi D.-L.;
 RT "The C-terminal cytoplasmic Lys-Thr-X-X-Trp motif in frizzled
 receptors mediates Wnt/beta-catenin signalling.";
 RL EMBO J. 19:4944-4954(2000).
 CC -!- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 are coupled to the beta-catenin canonical signaling pathway, which
 leads to the activation of dishevelled proteins, inhibition of
 GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 of Wnt target genes. A second signaling pathway involving PKC and
 calcium fluxes has been seen for some family members, but it is
 not yet clear if it represents a distinct pathway or if it can be
 integrated in the canonical pathway, as PKC seems to be required
 for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 to involve interactions with G-proteins. May be involved in
 transduction and intercellular transmission of polarity
 information during tissue morphogenesis and/or in differentiated
 tissues. According to Ref.2: Interacts specifically with Wnt8B but
 not with Wnt8 to induce the canonical beta-catenin pathway. Can
 also act in the Wnt pathway involving the activation of PKC, when
 overexpressed. According to Ref.4: Activated by Wnt8B, but does
 not synergize with Wnt5A or Wnt11. According to Ref.7: Activated
 by Wnt5A. According to Ref.3: binds to Wnt11.
 CC -!- TISSUE SPECIFICITY: In the embryo, expressed in the heart,
 pronephros and otic vesicles.
 CC -!- DEVELOPMENTAL STAGE: Present in unfertilized eggs, persisting
 through cleavage stages. Levels rise through gastrula (localized
 to the presumptive neuroectoderm and deep cells of the involuting
 mesoderm) and neurula stages (localized to the neural folds in
 presumptive neural-crest-cell-derived areas), peaking at the
 tailbud stage (detected in the eye, heart regions, pharyngeal
 arches and pronephros).
 CC -!- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of
 the Wnt/beta-catenin signaling pathway (By similarity).
 CC -!- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
 similarity).
 CC -!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 RECEPTORS.

CC -!- SIMILARITY: CONTAINS 1 FRIZZLED (Fz) DOMAIN.
 CC -----
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 CC -----
 DR EMBL; AF159106; AAD44331.1; -;
 DR EMBL; AF179213; AAD52671.1; -;
 DR EMBL; AJ243323; CAB45875.1; -;
 DR EMBL; AF114151; AAD21247.1; -;
 DR EMBL; AF039215; AAF63152.1; -;
 DR InterPro: IPR000539; Frizzled.
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR000832; GPCR_secretin.
 DR Pfam: PF01392; Fz; 2.
 DR Pfam: PF01534; Frizzled; 2.
 DR PRINTS: PR00489; FRIZZLED.
 DR SMART: SM00063; FRI; 1.
 DR PROSITE: PS00038; Fz; 1.
 DR PROSITE: PS0261; G-PROTEIN_RECEP_F2.4; 1.
 KW Multigene family; G-protein coupled receptor; Transmembrane;
 FT Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 549
 FT DOMAIN 23 231
 FT TRANSMEM 232 252
 FT DOMAIN 253 263
 FT TRANSMEM 264 284
 FT DOMAIN 285 311
 FT TRANSMEM 312 332
 FT DOMAIN 333 354
 FT TRANSMEM 355 375
 FT DOMAIN 376 398
 FT TRANSMEM 399 419
 FT DOMAIN 420 445
 FT TRANSMEM 446 466
 FT DOMAIN 467 503
 FT TRANSMEM 504 524
 FT DOMAIN 525 549
 FT DOMAIN 549 549
 FT SITE 527 532
 FT SITE 547 549
 FT CARBOHYD 51 51
 FT CARBOHYD 152 152
 FT CONFLICT 1 4
 FT CONFLICT 11 11
 FT CONFLICT 11 11
 FT CONFLICT 166 169
 FT CONFLICT 189 189
 FT CONFLICT 196 196
 FT CONFLICT 240 240
 FT CONFLICT 333 333
 FT CONFLICT 370 370
 FT CONFLICT 395 395
 FT CONFLICT 410 410
 FT CONFLICT 481 481
 FT CONFLICT 485 485
 FT CONFLICT 540 540
 SQ SEQUENCE 549 AA; 62119 MW; DA44954BFF8F594B CRC64;
 Query Match 16.4%; Score 308.5; DB 1; Length 549;
 Best Local Similarity 35.3%; Pred. No. 2.5e-18;
 Matches 73; Conservative 27; Mismatches 70; Indels 37; Gaps 8;
 QY 1 MFSLTILVCLMLHLALGVGAP-----CEAVRIPMCRHMPNITRMNHLHHSQENA 54
 DB 8 LFCLFLQQLCPSAQOYHGKIGISVPDHGCPISPTCTDIAYNQITMNPNLGHTNQEDA 67
 QY 55 ILAIEQYELVDVNCNSAVLRFFFFCAMYPACTLFLHDPKPKCKSVQCARDDCEPLMKM 114

FT SITE	620	625	LYS-THR-X-X-X-TRP MOTIF.
FT SITE	640	642	PDZ-BINDING.
FT CARBOHYD	125	125	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	226	226	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT	341	341	P -> R (IN REF. 2).
FT CONFLICT	352	352	S -> F (IN REF. 2).
FT SQ	SEQUENCE	642 AA;	70955 MW; 0AADC0C0DC820B6CE CRC64;
Query Match			
Best Local Similarity 37.68; Pred. No. 3.7e-18;			
Matches 64; Conservative 24; Mismatches 39; Indels 43; Gaps			
QY	9	LCLWL--HLALGVRG--	-----AP-----CEAVR 28
Ddb	56	LLWLLEAPLLGVRAQAAGVSGPQQAPPPQPGSQGOYNGERGISIPDHGYCQPI	115
QY	29	IPMCRHPMNITRPNHLHSTQENAILAIEQYELVDVNCASVLRFFFCAMVAPICTLE	88
		: : : : : : : : : : :	
Ddb	116	IPLCOTMAYNOTIMPLNGLHTNQEDAGLEVHOFYPLVKVQCSABELKFLCSWYAPGCTV-	174
QY	89	FUHDPIKPKSCVQRARDCEPLMKMYNHSWPESLACDELPLYDRG-VCI	137
		: : : : : : : : :	
Ddb	175	-LEQALPCRSICERAROGCCALMNKFGQWPDTLKCEKFPVHGAGELCV	223
RESULT 12			
FZD7_CHICK			
ID	FZD7_CHICK	STANDARD;	PRT: 567 AA.
AC	OS3329; Q9JIA04;		
RC	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DE	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Frizzled 7 precursor (Frizzled-7) (Fz-7) (cfZ-7).		
OS	FZD7 OR FZ7.		
GN	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RN	[1]		
RC	SEQUENCE FROM N.A.		
RP	TISSUE=Limb bud;		
RC	MEDLINE=98260739; PubMed=9598377;		
RA	Kengaku M., Twombly V., Tabin C.;		
RA	"Expression of Wnt and Frizzled genes during chick limb bud		
RT	development.";		
RT	Cold Spring Harb. Symp. Quant. Biol. 62:421-429(1997).		
RL	[2]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE=Embryo;		
RC	MEDLINE=20245319; PubMed=10781956;		
RA	Stark M.R., Biggs J.J., Schoenwolf G.C., Rao M.S.;		
RA	"Characterization of avian frizzled genes in cranial placode		
RT	development.";		
RT	Mech. Dev. 93:195-200(2000).		
CC	-!- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors		
CC	are coupled to the beta-catenin canonical signaling pathway, which		
CC	leads to the activation of dishevelled proteins, inhibition of		
CC	GSK-3 kinase, nuclear accumulation of beta-catenin and activation		
CC	of Wnt target genes. A second signaling pathway involving PKC and		
CC	calcium fluxes has been seen for some family members, but it is		
CC	not yet clear if it represents a distinct pathway or if it can be		
CC	integrated in the canonical pathway, as PKC seems to be required		
CC	for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem		
CC	to involve interactions with G-proteins. May be involved in		
CC	transduction and intercellular transmission of polarity		
CC	information during tissue morphogenesis and/or in differentiated		
CC	tissues.		
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-!- TISSUE SPECIFICITY: Expressed broadly in cranial ectoderm. Also		
CC	expressed in the developing somites and in other cranial placodes,		
CC	including the olfactory, lens, otic placodes (lateral half of the		
CC	vesicle) and epibranchial placodes. Low level of expression in all		

the mesoderm derivatives in the limb buds.

-1- DEVELOPMENTAL STAGE: First detected as stage 6 in the forming neural tube and somites, but not in trunk surface ectoderm. By stage 8, expression persists in the cranial ectoderm and is upregulated in the presumptive olfactory placodes. By stages 11-12, expression declines in the neural tube, but not in the cranial ectoderm; in somites, expressed all along the rostral-caudal axis as well as in presomital mesenchyme caudal to the developing somites. Lens and otic placode expression first visible at stage 12, strongest at stages 13-16. Detected uniformly in ectoderm and mesenchyme of the limb primordia at stage 17. By stage 18, decrease of ectodermal, otic, lens and olfactory placode expression; expression appears in the epibranchial placodes. By stages 22-30, highest levels in the most distal mesoderm of the autopod, in the ventricular zone of the neural tube from the forebrain to the spinal cord, in the dermomyotomes and the tail buds.

-1- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity).

-1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).

-1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.

-1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

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EMBL: AF031831; AAB87969.1; -
 EMBL: AF224317; AAF61097.1; -
 InterPro: IPR000539; Frizzled.
 InterPro: IPR000024; Fz_domain.
 InterPro: IPR000832; GPCR_secretin.
 Pfam: PF01392; Fz; 1.
 Pfam: PF01534; Frizzled; 1.
 PRINTS: PR00489; FRIZZLED.
 SMART: SK00063; FRI; 1.
 PROSITE: PS50038; Fz; 1.
 PROSITE: PS50261; G-protein coupled receptor; Transmembrane;
 Multigene family; G-protein coupled receptor; Signal.
 SIGNAL 1 31 POTENTIAL.
 CHAIN 32 567 FRIZZLED 7.
 DOMAIN 32 250 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 251 271 1 (POTENTIAL).
 DOMAIN 272 282 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 283 303 2 (POTENTIAL).
 DOMAIN 304 330 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 331 351 3 (POTENTIAL).
 DOMAIN 352 373 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 374 394 4 (POTENTIAL).
 DOMAIN 395 417 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 418 438 5 (POTENTIAL).
 DOMAIN 439 464 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 465 485 6 (POTENTIAL).
 DOMAIN 486 521 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 522 542 7 (POTENTIAL).
 DOMAIN 543 567 CYTOPLASMIC (POTENTIAL).
 DOMAIN 42 161 FZ.
 SITE 545 550 LYS-THR-X-X-TRP MOTIF.
 SITE 565 567 PDZ-BINDING.
 CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CONFLICT 34 35 HE -> OD (IN REF. 2).
 CONFLICT 480 480 V -> L (IN REF. 2).
 SEQUENCE 567 AA; 62811 MW; 3EFF0361FC899BC3 CRC64;

Query Match

16.3%; Score 306; DB 1; Length 567;

Best Local Similarity 39.2%; Pred. No. 4.2e-18;
 Matches 62; Conservative 23; Mismatches 47; Indels 26; Gaps 5;

QY 12 WLHLA---LGVRCAPCEA-----VRIPMCRHMPNITRMPNHLHST 50
 DB 14 WLGLAALLAALLGTCAAAHEDKATSVDPHGFQCPISIPLCYDIAYNTILNLLGHTN 73
 QY 51 QENAILAIEQYEELVDVNCSAVLRRFFFCAMYPATICTLEFLHDPKPKCKVCQRARDCEP 110
 DB 74 QEDAGLEVHGFYFLVKVQCSAELKFFLCSSMYAPVCTV--LEQAIPCRSLCERARQCEA 131
 QY 111 LMKMYNHSWPESLACDELPHYDRG-VCISPEAIVTDLP 147
 DB 132 LMKNGFQWPERLRCENFPVHGAGEICVGQN--TSDAP 167

RESULT 13
 FZD8_XENLA
 ID FZD8_XENLA STANDARD; PRT; 581 AA.
 AC O93274; Q9YI55;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Frizzled 8 precursor (Frizzled-8) (Fz-8) (Xfz8).
 GN FZ8.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A., AND COUPLING TO BETA-CATENIN PATHWAY.
 RC TISSUE=Embryo;
 RX PubMed=9651509;
 RA Itoh K., Jacob J., Sokol S.Y.;
 RT "A role for Xenopus Frizzled 8 in dorsal development.";
 RL Mech. Dev. 74:145-157(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=98301424; PubMed=9636083;
 RA Deardorff M.A., Tan C., Conrad L.J., Klein P.S.;
 RT "Frizzled-8 is expressed in the Spemann organizer and plays a role in early morphogenesis.";
 RL Development 125:2687-2700(1998).
 CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues. Activation by Wnt8, Wnt5A or Wnt3A induces expression of beta-catenin target genes. Displays an axis-inducing activity.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DEVELOPMENTAL STAGE: First expressed at high levels in the late blastula stages. At early gastrula, expressed in the deep cells of the Spemann organizer prior to involution of the dorsal blastopore lip. Detected in presumptive neurectoderm as gastrulation proceeds. Becomes restricted to the anterior ectoderm by the end of gastrulation. At neurula stages, localized in the most anterior region of the embryo, mainly in the anterior ectoderm including telencephalic and cement gland regions.
 CC -1- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity).
 CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED

more evident at stage 16. At stage 17, seen in the ectoderm and mesenchyme of the limb primordia. Detected at stage 20 in the lip of the optic cup, in the mesenchyme surrounding the eye, in the ectoderm overlying the lens and in the ectoderm caudal and ventral of the olfactory placodes. From stages 20-30, expressed in cartilage and in the dermomyotomes and migrating sclerotomal cells forming vertebrae.

CC -!- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity).

CC -!- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).

CC -!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.

CC -!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

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CC -----

DR EMBL: AF031830; AAB87968.1; -.

DR EMBL: AF224314; AAF61094.1; -.

DR InterPro: IPR000539; Frizzled.

DR InterPro: IPR000024; Fz_domain.

DR InterPro: IPR000832; GPCR_secretin.

DR Pfam: PF01392; Fz; 1.

DR Pfam: PF01392; Frizzled; 2.

DR SMART: SM00063; FRI; 1.

DR PROSITE: PS50038; FZ; 1.

DR PROSITE: PS50261; G-PROTEIN_RECEP_F2_4; 1.

KW Multigene family; G-protein coupled receptor; Transmembrane;

KW Developmental protein; Glycoprotein; Signal.

FT SIGNAL 1 48 POTENTIAL.

FT -CHAIN 49 592 FRIZZLED 1.

FT DOMAIN 49 271 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 272 292 1 (POTENTIAL).

FT TRANSMEM 293 303 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 304 324 2 (POTENTIAL).

FT -DOMAIN 325 351 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 352 372 3 (POTENTIAL).

FT DOMAIN 373 394 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 395 415 4 (POTENTIAL).

FT DOMAIN 416 438 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 439 459 5 (POTENTIAL).

FT DOMAIN 460 485 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 486 506 6 (POTENTIAL).

FT DOMAIN 507 546 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 547 567 7 (POTENTIAL).

FT DOMAIN 568 592 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 65 184 FZ.

FT SITE 570 575 LYS-THR-X-X-TRP MOTIF.

FT SITE 590 592 PDZ-BINDING.

FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 533 533 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 592 AA: 65490 MW: 933E76063CA6109D CRC64;

Query Match 16.3%; Score 305.5; DB 1; Length 592;

Best Local Similarity 42.9%; Pred. No. 4.9e-18;

Matches 57; Conservative 25; Mismatches 42; Indels 9; Gaps 3;

QY 16 ALGVRCAP-----CEAVRTPMCRHMPWNTTRPNHLHSTQENALAIQYEELVDVNC 69

DB 56 ALSGRGISPDHGVCQIPISPLCTDIAYNOTIMPNLGHTNQEDAGLEVHQFPLVQVC 115

QY 70 SAVLRPFECAMYPICLTLEFLHPDKPKSVQCORARDCEPLMKMYNHWSPESLACDEL 129

DB 116 SAELKFLCSMYAPVCTV--LEQALPCCRSLCERARQCCALMNKFGQWPDLRCEKFP 173

QY 130 VYDRG-VCISPEA 141

DB 174 VHAGELCVGQNA 186

RESULT 15

FZD8_MOUSE

ID FZD8_MOUSE STANDARD; PRT; 685 AA.

AC Q61091;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Frizzled 8 precursor (Frizzled-8) (Fz-8) (mFz8).

GN FZD8.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96224032; PubMed=8626800;

RA Wang Y., Macke J.P., Abella B.S., Andreasson K., Worley P.,

RA Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;

RT "A large family of putative transmembrane receptors homologous to the product of the Drosophila tissue polarity gene frizzled.";

RL J. Biol. Chem. 271:4468-4476(1996).

RN [2]

RP COUPLING TO BETA-CATENIN PATHWAY.

RX MEDLINE=99324245; PubMed=10395542;

RA Sheidahl L.C., Park M., Malbon C.C., Moon R.T.;

RT "Protein kinase C is differentially stimulated by Wnt and Frizzled homologs in a G-protein-dependent manner.";

RT Curr. Biol. 9:695-698(1999).

RL CC -!- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins. Inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues. Activation by Wnt8 induces expression of beta-catenin target genes.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: Expressed in chondrocytes.

CC -!- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity).

CC -!- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).

CC -!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.

CC -!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

CC -----

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CC -----

DR EMBL: U43321; AAC52433.1; -.

DR MGD; MGI:108460; Fzd8.

DR InterPro: IPR000539; Frizzled.

DR InterPro: IPR000024; Fz_domain.

DR InterPro: IPR000832; GPCR_secretin.

DR Pfam: PF01392; Fz; 1.

DR Pfam: PF01392; Frizzled; 1.

DR PRINTS; PR00489; FRIZZLED.

DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50261; G-PROTEIN_RECEP_F2_4; 1.
KW Multigene family; G-protein coupled receptor; Transmembrane;
KW Developmental protein; Glycoprotein; Signal.
FT SIGNAL 1 27
FT CHAIN 28 685
FT DOMAIN 28 272
FT TRANSMEM 273 293
FT DOMAIN 294 309
FT TRANSMEM 310 330
FT DOMAIN 331 394
FT TRANSMEM 395 415
FT DOMAIN 416 437
FT TRANSMEM 438 458
FT DOMAIN 459 481
FT TRANSMEM 482 502
FT DOMAIN 503 530
FT TRANSMEM 531 551
FT DOMAIN 552 582
FT TRANSMEM 583 603
FT DOMAIN 604 685
FT DOMAIN 604 685
FT DOMAIN 30 151
FT DOMAIN 168 173
FT DOMAIN 353 361
FT DOMAIN 640 654
FT SITE 606 611
FT SITE 683 685
FT CARBOHYD 49 49
FT CARBOHYD 152 152
FT CARBOHYD 473 473
SQ SEQUENCE 685 AA; 73215 MW; F333B49474411267 CRC64;

Query Match 16.2%; Score 305; DB 1; Length 685;
Best Local Similarity 39.5%; Pred. No. 6.4e-18;
Matches 58; Conservative 31; Mismatches 46; Indels 12; Gaps 5;
QY 4 SILVALCLHLALGVGA-----PCEAVRIPMCRHMPWNITRMPNHLHSHSTQENAILAI 58
Db 11 SLAALAV-LQRSSGAAASAKELACQETVPLCKGIGYNYTMPNQFNHDTQDEAGLEV 69
QY 59 EOYEELVDVNCNAVLRFFFCAMYPACTLEFLHDPIKPKCKSVQCRARDCEPLMKMYNHS 118
Db 70 HQFWPLVEIQCSPLDKFFLCSMYTPIC-LEDYKKPLPPCRSVCKERAKAGCAPLMROYGFA 128
QY 119 WPESLACDELVPYDRGVCISPEAIVTD 145
Db 129 WPDNRCDRLP--EOG---NPDTLCMD 150

Search completed: March 7, 2003, 11:24:18
Job time : 16 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2003, 11:20:59 ; Search time 35 Seconds
(without alignments)
2036.923 Million cell updates/sec

Title: US-09-909-775-2

Perfect score: 1879

Sequence: 1 MFLSILVALCLWLHLALGVR.....SPKNIKTRSAQKRTNPKRV 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organalle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1879	100.0	346	4	O14877
2	1746.5	92.9	351	11	Q921N6
3	1732	92.2	348	11	Q9JLS5
4	1720	91.5	348	11	Q35222
5	1485	79.0	303	11	Q924N2
6	1030	54.8	197	11	Q9JLS4
7	829	44.1	323	11	Q91W58
8	828	44.1	315	13	Q9IA95
9	822.5	43.8	319	13	P79993
10	816	43.4	318	13	P79936
11	799	42.5	315	13	Q9W6E0
12	791	42.1	148	11	Q91ZX9
13	673.5	35.8	213	13	Q9PTD9
14	621.5	33.1	261	11	O08570
15	512	27.2	130	6	Q95JB1
16	482.5	25.7	138	13	Q9PTN5

17	318.5	17.0	577	13	Q918V7	Q918V7 brachydanio
18	318.5	17.0	579	13	Q9Y100	Q9Y100 brachydanio
19	318.5	17.0	579	13	Q9W6E4	Q9W6E4 brachydanio
20	317.5	16.9	579	13	Q9PTT7	Q9PTT7 brachydanio
21	312	16.6	591	4	Q8TAN2	Q8TAN2 homo sapien
22	303.5	16.2	559	13	Q90ZT3	Q90ZT3 brachydanio
23	302.5	16.1	559	13	Q98S12	Q98S12 brachydanio
24	302	16.1	576	13	Q9Y149	Q9Y149 brachydanio
25	302	16.1	576	13	Q9PWK6	Q9PWK6 brachydanio
26	302	16.1	576	13	Q9PNW8	Q9PNW8 brachydanio
27	301.5	16.0	557	13	Q8QFM3	Q8QFM3 brachydanio
28	300.5	16.0	550	13	Q90Y17	Q90Y17 brachydanio
29	298.5	15.9	574	4	Q96B74	Q96B74 homo sapien
30	291	15.5	592	13	Q9W6E2	Q9W6E2 brachydanio
31	283	15.1	568	5	O16147	O16147 caenorhabdi
32	279	14.8	550	5	Q9U8U6	Q9U8U6 caenorhabdi
33	268.5	14.3	580	13	Q9PTT8	Q9PTT8 brachydanio
34	268.5	14.3	580	13	Q9W6E3	Q9W6E3 brachydanio
35	268.5	14.3	580	13	Q90WN3	Q90WN3 brachydanio
36	265	14.1	537	4	Q8TAV8	Q8TAV8 homo sapien
37	257.5	13.7	545	5	Q9U322	Q9U322 hydra attien
38	248	13.2	295	13	Q91897	Q91897 xenopus lae
39	247.5	13.2	920	5	Q95P13	Q95P13 strongyloce
40	237.5	12.6	525	5	Q10662	Q10662 caenorhabdi
41	237.5	12.6	529	5	Q9N532	Q9N532 caenorhabdi
42	233	12.4	313	4	O00546	O00546 homo sapien
43	232.5	12.4	281	13	Q73821	Q73821 xenopus lae
44	230	12.2	308	6	O19116	O19116 bos taurus
45	230	12.2	314	11	O08861	O08861 mus musculu

ALIGNMENTS

RESULT 1

O14877 ID O14877 PRELIMINARY: PRT; 346 AA.

AC O14877;
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE FrpHE.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=ENDOMETRIUM;

RA Abu-Jawdeh G.M., Comella N., Brown L.F., Tognazzi K., Kocher O.;

RT "frizzled related protein frpHE (Homo Sapiens).";

RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF026692; AAC04617.1; .

DR InterPro; IPR000024; Fz_domain.

DR InterPro; IPR001134; Netrin_C.

DR Pfam; PF01392; Fz; 1.

DR Pfam; PF01759; NTR; 1.

DR SMART; SM00063; FRI; 1.

DR PROSITE; PS50038; Fz; 1.

SQ SEQUENCE 346 AA; 39860 MW; 75D78D43E444CC2A CRC64;

Query Match

Best Local Similarity 100.0%; Score 1879; DB 4; Length 346;

Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRPNHLHHSTQENAILAIEQ 60

|||||

Db 1 MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRPNHLHHSTQENAILAIEQ 60

QY 61 YEELVDVNC SAVLRFFFCFAMYPICITLPLHDPKPSVCORARDDCEPLMKMYNHSWP 120

|||||

Db 61 YEELVDVNC SAVLRFFFCFAMYPICITLPLHDPKPSVCORARDDCEPLMKMYNHSWP 120

QY 121 ESLACDELPHYDGVGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVCCKRLSPDRCKC 180
DB 121 ESLACDELPHYDGVGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVCCKRLSPDRCKC 180
QY 181 KVKVPTLATYLSKNYSYVIHAKIKAVORSGCNEVTTVDVKKEIFKSSSPIPTQVPLITN 240
DB 181 KVKVPTLATYLSKNYSYVIHAKIKAVORSGCNEVTTVDVKKEIFKSSSPIPTQVPLITN 240
QY 241 SSCQCCHILPHQDVLIMCYEWSRMMLENCLEKVRDQLSKRISQWEERLQORRTVD 300
DB 241 SSCQCCHILPHQDVLIMCYEWSRMMLENCLEKVRDQLSKRISQWEERLQORRTVD 300
QY 301 KKTAGTSSRNPCKGPKPPAPKSPKKNITKRSQAOKRTNPKRV 346
DB 301 KKTAGTSSRNPCKGPKPPAPKSPKKNITKRSQAOKRTNPKRV 346

RESULT 2

Q9ZIN6 PRELIMINARY; PRT; 351 AA.
AC Q9ZIN6;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE Secreted frizzled-related sequence protein 4.
GN SFRP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang J.T., Esumi N., Moore K., Li Y., Zhang S., Chew C., Goodman B.,
RA Ratner A., Moody S., Stetten G., Campochiaro P.A., Zack D.J.;
RT "Cloning and characterization of a secreted frizzled-related protein
RT that is expressed by the retinal pigment epithelium.";
RL Hum. Mol. Genet. 0:0-0(1999).
DR -EMBL; AF117709; AAD12306.1; -;
DR MGI; 892010; Sfrp4.
DR InterPro: IPR000024; Fz_domain.
DR Netrin_C.
DR Pfam: PF01392; Fz; 1.
DR Pfam: PF01759; NTR; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; P550038; FZ; 1.
SQ SEQUENCE 351 AA; 40342 MW; 6CB0B625920A54FE CRC64;

Query Match 92.9%; Score 1746.5; DB 11; Length 351;
Best Local Similarity 92.5%; Pred. No. 9.2e-152;
Matches 322; Conservative 9; Mismatches 14; Indels 3; Gaps 1;
QY 1 MFLSILVALCLWLHLAGVGRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60
DB 1 MFLSILVALCLWLHLAGVGRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60
QY 61 YEELVDVNCSSVLRFFFCAMYPACTLEFLHDPDKCKSVQCORARDDCEPLMKMYNHSWP 120
DB 61 YEELVDVNCSSVLRFFFCAMYPACTLEFLHDPDKCKSVQCORARDDCEPLMKMYNHSWP 120
QY 121 ESLACDELPHYDGVGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVCCKRLSPDRCKC 180
DB 121 ESLACDELPHYDGVGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVCCKRLSPDRCKC 180
QY 181 KVKVPTLATYLSKNYSYVIHAKIKAVORSGCNEVTTVDVKKEIFKSSSPIPTQVPLITN 240
DB 181 KVKVPTLATYLSKNYSYVIHAKIKAVORSGCNEVTTVDVKKEIFKSSSPIPTQVPLITN 240
QY 241 SSCQCCHILPHQDVLIMCYEWSRMMLENCLEKVRDQLSKRISQWEERLQORRTVD 300
DB 241 SSCQCCHILPHQDVLIMCYEWSRMMLENCLEKVRDQLSKRISQWEERLQORRTVD 300
QY 301 KKTAGTSSRNPCKGPKPPAPKSPKKNITKRSQAOKRTNPKRV 346
DB 301 KKTAGTSSRNPCKGPKPPAPKSPKKNITKRSQAOKRTNPKRV 346

DB 301 KKOIASRTSRTSRNPCKSGRPPAPKSPKKNIKARSAPKKSNLKK 348

RESULT 3

Q9JLS5 PRELIMINARY; PRT; 348 AA.
AC Q9JLS5;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Frizzled related protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISHER;
RX MEDLINE=21378144; PubMed=11485313;
RA Yam J.W.P., Chan K.W., Wong V.K.W., Hsiao W.L.W.;
RT "Transcriptional activity of the promoter region of rat frizzled-
RT related protein gene.";
RL Biochem. Biophys. Res. Commun. 286:94-100(2001).
DR EMBL; AF140346; AAF66480.1; -;
DR InterPro: IPR000024; Fz_domain.
DR Netrin_C.
DR Pfam: PF01392; Fz; 1.
DR Pfam: PF01759; NTR; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; P550038; FZ; 1.
SQ SEQUENCE 348 AA; 39718 MW; 6CA7979D5A6CA97 CRC64;

Query Match 92.2%; Score 1732; DB 11; Length 348;
Best Local Similarity 92.5%; Pred. No. 1.9e-150;
Matches 319; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 1 MFLSILVALCLWLHLAGVGRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60
DB 1 MFLSILVALCLWLHLAGVGRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60
QY 61 YEELVDVNCSSVLRFFFCAMYPACTLEFLHDPDKCKSVQCORARDDCEPLMKMYNHSWP 120
DB 61 YEELVDVNCSSVLRFFFCAMYPACTLEFLHDPDKCKSVQCORARDDCEPLMKMYNHSWP 120
QY 121 ESLACDELPHYDGVGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVCCKRLSPDRCKC 180
DB 121 ESLACDELPHYDGVGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVCCKRLSPDRCKC 180
QY 181 KVKVPTLATYLSKNYSYVIHAKIKAVORSGCNEVTTVDVKKEIFKSSSPIPTQVPLITN 240
DB 181 KVKVPTLATYLSKNYSYVIHAKIKAVORSGCNEVTTVDVKKEIFKSSSPIPTQVPLITN 240
QY 241 SSCQCCHILPHQDVLIMCYEWSRMMLENCLEKVRDQLSKRISQWEERLQORRTVD 300
DB 241 SSCQCCHILPHQDVLIMCYEWSRMMLENCLEKVRDQLSKRISQWEERLQORRTVD 300
QY 301 KKTAGTSSRNPCKGPKPPAPKSPKKNIKARSAPKKSNLKK 345
DB 301 KKTAGTSSRNPCKGPKPPAPKSPKKNIKARSAPKKSNLKK 345

RESULT 4

O35222 PRELIMINARY; PRT; 348 AA.
AC O35222;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Frizzled related protein frpAP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

```

RN  [1]
RC  SEQUENCE FROM N.A.
RC  STRAIN=SPRAGUE-DAWLEY;
RA  Wolf V., Artuso L., Dharmarajan A., Guo K., Bielke W., Friis R.R.;
RT  "A frizzled related gene is upregulated in Physiological Apoptosis.";
RL  Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN  [2]
RC  SEQUENCE FROM N.A.
RC  STRAIN=SPRAGUE-DAWLEY;
RA  Guo K., Wolf V., Dharmarajan A., Feng Z., Bielke W., Susanne S.,
RA  Friis R.R.;
RT  "Apoptosis-associated Gene Expression in Corpus luteum of the Rat.";
RL  Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF012891; AAB65431.1; -.
DR  InterPro: IPR000024; Fz_domain.
DR  InterPro: IPR001134; Netrin_C.
DR  Pfam: PF01392; Fz; 1.
DR  Pfam: PF01759; NTR; 1.
DR  SMART; SM00063; FRI; 1.
DR  PROSITE; PS50038; FZ; 1.
SQ  SEQUENCE 348 AA; 39735 MW; 08BA5BF909AE7B64 CRC64;

Query Match          91.5%; Score 1720; DB 11; Length 348;
Best Local Similarity 92.2%; Pred. No. 2.4e-149;
Matches 318; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

Qy  1 MFLSTLVALCLWLHLALGVGAPCEAVRIPMCRHHPWNITRPNHLHSTQENAILAEQ 60
Db  1 MLLSTLVALCLVRLALGVGAPCEAVRIPMCRHHPWNITRPNHLHSTQENAILAEQ 60

Qy  61 YEELDVNCSAVLRFFFFCAMYPACTLEFLHDPKPKSVQARDDCEPLMKMYNHSWP 120
Db  61 YEELDVNCSVLSFFLCAMYPACTLEFLHDPKPKSVQARDDCEPLMKMYNHSWP 120

Qy  121 ESLACDELVPYDRGVCISPEAIVTDLPEVKWIDITPDMWQERLVDVCKLSPOKCK 180
Db  121 ESLACDELVPYDRGVCISPEAIVTDLPEVKWIDITPDMWQERLVDVCKLSPOKCK 180

Qy  181 KVKPPTLATYLSKNYSYVIHAKIKAVQSGCNEVTVVDVKEIFKSSSPIPRTQVPLTN 240
Db  181 KVKPPTLATYLSKNYSYVIHAKIKAVQSGCNEVTVVDVKEIFKSSSPIPRTQVPLTN 240

Qy  241 SSCQCPHILPHODVLIMCYEWSRMMLLENCLVEKWRDLSRRS 345
Db  241 SSCQCPHILPHODVLIMCYEWSRMMLLENCLVEKWRDLSRRS 345

Qy  301 KKKTAGTSRNPAPKPGPPAPKASPKNKIKTSQAQRTPKR 345
Db  301 KKQIASRTSRNPAPKPGRSAPKSPAPKKNKIKARSAPKSNPK 345

RESULT 5
Q924N2 ID Q924N2 PRELIMINARY; PRT; 303 AA.
AC Q924N2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Frizzled related protein.
GN FRP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RA Chan K.W., Yam J.W.P., Hsiao W.W.L.;
RT "Brain specific rat frizzled related protein gene.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220608; AAK59511.1; -.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR001134; Netrin_C.
DR Pfam: PF01392; Fz; 1.

us-09-909-775-2.rspt
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DR Pfam: PF01759; NTR; 1.
DR PROSITE; PS50038; FZ; 1.
SQ SEQUENCE 303 AA; 34507 MW; 8AB612A48933AAE1 CRC64;

Query Match          79.0%; Score 1485; DB 11; Length 303;
Best Local Similarity 96.1%; Pred. No. 6.7e-128;
Matches 273; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy  1 MFLSTLVALCLWLHLALGVGAPCEAVRIPMCRHHPWNITRPNHLHSTQENAILAEQ 60
Db  1 MLLSTLVALCLWLRLALGVGAPCEAVRIPMCRHHPWNITRPNHLHSTQENAILAEQ 60

Qy  61 YEELDVNCSAVLRFFFFCAMYPACTLEFLHDPKPKSVQARDDCEPLMKMYNHSWP 120
Db  61 YEELDVNCSVLSFFLCAMYPACTLEFLHDPKPKSVQARDDCEPLMKMYNHSWP 120

Qy  121 ESLACDELVPYDRGVCISPEAIVTDLPEVKWIDITPDMWQERLVDVCKLSPOKCK 180
Db  121 ESLACDELVPYDRGVCISPEAIVTDLPEVKWIDITPDMWQERLVDVCKLSPOKCK 180

Qy  181 KVKPPTLATYLSKNYSYVIHAKIKAVQSGCNEVTVVDVKEIFKSSSPIPRTQVPLTN 240
Db  181 KVKPPTLATYLSKNYSYVIHAKIKAVQSGCNEVTVVDVKEIFKSSSPIPRTQVPLTN 240

Qy  241 SSCQCPHILPHODVLIMCYEWSRMMLLENCLVEKWRDLSRRS 284
Db  241 SSCQCPHILPHODVLIMCYEWSRMMLLENCLVEKWRDLSRRS 284

RESULT 6
Q9JLS4 ID Q9JLS4 PRELIMINARY; PRT; 197 AA.
AC Q9JLS4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Frizzled related protein (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=FISHER; TISSUE=LIVER;
RX MEDLINE=21378144; PubMed=11485313;
RA Yam J.W.P., Chan K.W., Wong V.K.W., Hsiao W.W.L.;
RT "Transcriptional activity of the promoter region of rat frizzled-
RT related protein gene.";
RL Biochem. Biophys. Res. Commun. 286:94-100(2001).
DR EMBL; AF140347; AAF66481.1; -.
DR InterPro: IPR000024; Fz_domain.
DR Pfam: PF01392; Fz; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
FT NON_TER 197 197
SQ SEQUENCE 197 AA; 22563 MW; CD4342B43B88692B CRC64;

Query Match          54.8%; Score 1030; DB 11; Length 197;
Best Local Similarity 94.9%; Pred. No. 1.8e-86;
Matches 187; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy  1 MFLSTLVALCLWLHLALGVGAPCEAVRIPMCRHHPWNITRPNHLHSTQENAILAEQ 60
Db  1 MLLSTLVALCLWLRLALGVGAPCEAVRIPMCRHHPWNITRPNHLHSTQENAILAEQ 60

Qy  61 YEELDVNCSAVLRFFFFCAMYPACTLEFLHDPKPKSVQARDDCEPLMKMYNHSWP 120
Db  61 YEELDVNCSVLSFFLCAMYPACTLEFLHDPKPKSVQARDDCEPLMKMYNHSWP 120

Qy  121 ESLACDELVPYDRGVCISPEAIVTDLPEVKWIDITPDMWQERLVDVCKLSPOKCK 180
Db  121 ESLACDELVPYDRGVCISPEAIVTDLPEVKWIDITPDMWQERLVDVCKLSPOKCK 180
```

QY 181 KVKPTLATYLSKNYSY 197
 DB 181 KVKPTLATYLSKNYSY 197

RESULT 7

Q91W58 PRELIMINARY; PRT; 323 AA.

AC Q91W58;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Frizzled-related protein.
 GN FRZB.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC016884; AAH16884.1; -;
 DR MCD; MGI:892032; Frzb.
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR001134; Netrin_C.
 DR Pfam; PF01392; Fz; 1.
 DR Pfam; PF01759; NTR; 1.
 DR PROSITE; PS50038; Fz; 1.
 SQ SEQUENCE 323 AA; 36039 MW; 3F144988CFC97740 CRC64;

Query Match 44.1%; Score 829; DB 11; Length 323;
 Best Local Similarity 51.1%; Pred. No. 8.2e-68;
 Matches 166; Conservative 49; Mismatches 76; Indels 34; Gaps 9;

QY 3 LSTLVALCLWLHALVGRGAPCEAVRIPMCRHMPNITRMPNHLHHSTQENAILAIEQYE 62
 DB 16 LLLVLAAL-LQVP-GAQAACAEVPRIPCKSLPWNMTKMPNHLHHSTQANAILAMEQFE 73
 QY 63 ELVDVNCASVLRFFFCAMYPACTLEFLHDPKPKSVQCARDDCEPLMKMYNHSWPES 122
 DB 74 GLLGTHCSPLDLLFLCAMYAPICTIDFQHEPKPKSVQCARARQGCCEPLIKYRHSWPES 133

QY 123 LACDELPHYDRGVCISPEAIVT---DLPEVKKWIDITPDMVQERPLVDCKRLSPDRCK 178
 DB 134 LACDELPHYDRGVCISPEAIVTADGADFPMDSS-----TCHCRGASSERC 178

QY 179 KCKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSS-SPIPRTOVPL 237
 DB 179 KCKPVRATQKTYPRNNYVIRAKVEKMK-CHDVTAVVEVKEILKASLVNIPROTVNL 237

QY 238 ITNSSCQCCHILPHQDVLMICY--EWSRMMLLENCLVEKWRDLSKRSIQWERLQ--- 292
 DB 238 YTTSGCLCPPLTNEEVINGYDEERSRLLLVEGSAEKWKDRLGKVKRWMDKRLHLG 297

QY 293 ----EQRRVTQDKKKTAGRTSRNP 313
 DB 298 LGKTDASDSTQNGK--SGRNSNRP 320

RESULT 8

Q91A95 PRELIMINARY; PRT; 315 AA.

AC Q91A95;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Frzb.
 GN FRZB.

OS Gallus gallus (Chicken)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20123838; PubMed=10656762;
 RA Ladhari R.K., Church V.L., Allen S., Robson L., Abdelfattah A.,
 RA Brown N.A., Hattersley G., Rosen V., Luyten F.P., Dale L.,
 RA Francis-West P.H.;
 RT "Cloning and Expression of the Wnt Antagonists Sfrp-2 and Frzb during Chick Development";
 RL Dev. Biol. 218:183-198(2000).
 DR EMBL; AF218057; AAF27643.1; -;
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR001134; Netrin_C.
 DR Pfam; PF01392; Fz; 1.
 DR Pfam; PF01759; NTR; 1.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PS50038; Fz; 1.
 SQ SEQUENCE 315 AA; 35003 MW; 6EBC58DB5335505D CRC64;

Query Match 44.1%; Score 828; DB 13; Length 315;
 Best Local Similarity 50.0%; Pred. No. 9.9e-68;
 Matches 162; Conservative 52; Mismatches 80; Indels 30; Gaps 6;

QY 4 SILVALCLWLHALVGRGAPCEAVRIPMCRHMPNITRMPNHLHHSTQENAILAIEQYEE 63
 DB 7 ALALAALLLGRAPAGRAAACEVPRIPCKSLPWNMTKMPNHLHHSTQANAILAMEQFEG 66

QY 64 LVDVNCASVLRFFFCAMYPACTLEFLHDPKPKSVQCARDDCEPLMKMYNHSWPESL 123
 DB 67 LGTNCSPDLLFLCAMYAPICTIDFQHEPKPKSVQCARARQGCCEPLIKYRHSWPESL 126

QY 124 ACDELPHYDRGVCISPEAIVT---DLPEVKKWIDITPDMVQERPLVDCKRLSPDRCK 179
 DB 127 ACDELPHYDRGVCISPEAIVTAEADFPMDSN-----NGNCRGTGIERCK 171

QY 180 CKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSS-SPIPRTOVPLI 238
 DB 172 CKPIKATQKTYPRNNYVIRAKVEK-KTKCHDVTAVVEVKEILKSSLVNIPKDTVNL 230

QY 239 ITNSSCQCCHILPHQDVLMICY--EWSRMMLLENCLVEKWRDLSKRSIQWERLQ--- 296
 DB 231 TNSGCLCPPLTNEEVINGYDEERSRLLLVEGSAEKWKDRLGKVKRWMDKRLH--- 287

QY 297 TVQDKKKTAGRTSRNSNPPKPKGP 320
 DB 288 ----LGKKGECQSDSALKTGPK 307

RESULT 9

P79993 PRELIMINARY; PRT; 319 AA.

AC P79993;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Frzb precursor.
 OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=97236496; PubMed=9118219;
 RA Wang S., Krinks M., Lin K., Luyten F.P., Moos M. Jr.;
 RT "Frzb, a secreted protein expressed in the Spemann organizer, binds and inhibits Wnt-8";
 RL Cell 88:757-766(1997).
 DR EMBL; U78598; AAC60114.1; -;
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR001134; Netrin_C.
 DR Pfam; PF01392; Fz; 1.

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Db 29 ASCPEVRIPCKSPMWNMTKPNHLHHSTQANAILAEQEGELLTTTECSQDILLFFTCAMY 88
Qy 82 APICTLEFLHDPIPKPKSCVQORADDCPELKMKNHNSWPESLACDELPPYDVGVCISPEA 141
Db 89 APICTIDFQHEPIPKPKSCVQERARAGEPILIKYRHTWPESLACEELPPYDVGVCISPEA 148
Qy 142 IVTDLPEDKWIDITPDMVMQERPLDYDCKRLSPDRCKCKVKKPTLATYLSKNYSYVHA 201
Db 149 IVT----VEQGTDSMPDFSMSNNGCGSGR--EHCKCKPMKATOKTYLKNKNYVIRA 201
Qy 202 KIKAVORSGCNEVTTVDVVKEIFKSS-SPIPTQVPLTNSSCQCCHILPHQDVLIMCYE 260
Db 202 KVKEV-KVKCHDAIYVEVKEILKSLVINPKDTVTLTNSGGLCPQLVANEESYITMGVE 260
Qy 261 --WFSRWMLLENCLVEKWRDOLSKRSIOWEERLQEQRRTVODKKKTAGRTSRNPFPKG 318
Db 261 DKERTRLLVEGSLAEKWRDLAKVKVRWQKLR-----PRKSK 300
Qy 319 KPPAKPASPKNKIKTRSAQ 338
Db 301 DPVAP---IPNKNNSRQAR 317

RESULT 11
Q9W6E0 PRELIMINARY; PRT; 315 AA.
AC Q9W6E0;
ID Q9W6E0;
AD Q9W6E0;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Fz b1.
GN FZB1.
DE FZB1.
OS Eukarydanio rerio (zebrafish) (Zebra danio).
OC Brachyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Futurani-Seiki M.;
RT "Cloning of zebrafish fzb-1, antagonist of Wnt signaling.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Shinya M., Driever W., Futurani-Seiki M.;
RL Shimada (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF116853; AA022462.1; .
DR ZFIN; ZDB-GENE-990715-1; fzb1.
DR InterPro; IPR000024; Fz_domain.
DR DR PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS00308; Fz; 1.
SQ SEQUENCE 315 AA; 36031 MW; 0F23DF09F9B9414 CRC64;

Query Match 42.5%; Score 799; DB 13; Length 315;
Best Local Similarity 50.2%; Pred. No. 4.5e-65;
Matches 155; Conservative 55; Mismatches 77; Indels 22; Gaps

Qy 1 MFLSILVALCLWLHALGVRGAPCAEVRIPCMRHPMNWITRMPNHLHHSTQANAILAEQ 60
Db 9 MFCIVLAFAL-LEIPRGTGAASCEPIRIPCKSPMWNMTKPNHLHHSTQANAILAEQ 67
Qy 61 YEELVDVNCNSAVLRFFPCAMYAPICTLEFLHDPIPKPKSCVQORADDCPELKMKNHNSWP 120
Db 68 FEGLLGTQCSADLLFFLCAMYAPICTIDFQHDPIPKPKSCVQERARAGEPILIKYRHTWP 127
Qy 121 ESLACDELPPYDVGVCISPEAIV-TDLPEDVKWIDI-----TPDMVMQERPLD---VD 160
Db 128 ESLACEELPPYDVGVCISPEAIVVAEGDINSYQDPKACNPEGNPDF-----PMSINTN 187
Qy 170 CKRLSPDRCKCKVKKPTLATYLSKNYSYVHAIKAKVQRSGCNEVTTVDVVKEIFKSS-S 228

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Db 183 CKGAN-DRCKCKSVFKQKTSKNNYVIRARVKEI-RIRNHDLSAIVEKVKLSLV 240
QY 229 PIPRTQVPLTNSQCQPHILPHODVLIMCY--EWRSMRLLENCLVEKWRDQSKRSIQ 286
Db 241 NIPRDTVTLVNSCLCPPLTANDEYIIMGYENERSRLLLIDRSIAQKWKIKGRVKR 300
QY 287 WEERLQQR 295
Db 301 WDQAANGRR 309

RESULT 12
Q91ZX9 PRELIMINARY; PRT; 148 AA.
AC Q91ZX9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Frizzled-related protein 4 (Fragment).
GN FRP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVCP;
RX MEDLINE=21378144; PubMed=11485313;
RA Yam J.W.P., Chan K.W., Wong V.K.W., Hsiao W.L.W.;
RT "Transcriptional activity of the promoter region of rat frizzled-
related protein gene.";
RL Biochem. Biophys. Res. Commun. 286:94-100(2001).
DR EMBL: AF364506; AAL14904.1; -.
DR InterPro: IPR000024; Fz_domain.
DR Pfam: PF01392; Fz; 1.
DR PROSITE: PSS0038; Fz; 1.
FT 'NON_TER 148 148
SQ SEQUENCE 148 AA; 16940 MW; 13D7CED1960B3092 CRC64;

Query Match 42.1%; Score 791; DB 11; Length 148;
Best Local Similarity 96.6%; Pred. No. 1e-64;
Matches 143; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFSLVALCLWLHLALGVGAPCEAVRIPMCRHMPNITRMPNHLHSHSTQENAILAIEQ 60
Db 1 MLRSILVALCLWLRLALGVGAPCEAVRIPMCRHMPNITRMPNHLHSHSTQENAILAIEQ 60
QY 61 YEELVDVNCNAVURFFFCAMYPACTLEFLHDPKCKVCQQRARDCEPLMKMWNHWP 120
Db 61 YEELVDVNCSSVLRFFLCAMYPACTLEFLHDPKCKVCQQRARDCEPLMKMWNHWP 120
QY 121 ESLACDELVDVDRGVCISPAIVTDLPE 148
Db 121 ESLACDELVDVDRGVCISPAIVTDLPE 148

RESULT 13
Q9PTD9 PRELIMINARY; PRT; 213 AA.
AC Q9PTD9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Secreted frizzled-related protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BREED WHITE LEGHORN;

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RA Baranski M., Berdougo E., Sandler J., Darnell D.K., Burrus L.W.;
RT "The Dynamic Expression Pattern of frzb-1 Suggests Multiple Roles in
Chick Development.";
RL Dev. Biol. 0:0-0(1999).
DR EMBL: AF207665; AAF20143.1; -.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR001134; Netrin_C.
DR Pfam: PF01392; Fz; 1.
DR Pfam: PF01759; NTR; 1.
DR SMART: SM00063; FRI; 1.
DR PROSITE: PSS0038; Fz; 1.
FT 'NON_TER 213 213
SQ SEQUENCE 213 AA; 23766 MW; E30E237339FD27E2 CRC64;

Query Match 35.8%; Score 673.5; DB 13; Length 213;
Best Local Similarity 56.1%; Pred. No. 8.7e-54;
Matches 128; Conservative 32; Mismatches 49; Indels 19; Gaps 4;

QY 37 WNITRPNHLHSHSTQENAILAIEQYELVDVNCNAVURFFFCAMYPACTLEFLHDPK 96
Db 1 WNITRPNHLHSHSTQENAILAIEQYELVDVNCNAVURFFFCAMYPACTLEFLHDPK 96
QY 97 CKSVQQRARDCEPLMKMWNHWPESLACDELVDVDRGVCISPAIVTDLPEVKKWIDIT 156
Db 61 CKSVQQRARDCEPLMKMWNHWPESLACDELVDVDRGVCISPAIVTDLPEVKKWIDIT 156
QY 157 PDMVQERPLDV---DCKRLSPORCKCKVKPTLATVLSKNYSYVIAKIKAVORSQNE 213
Db 115 -----PMSNNGCGGTGIERCKCKPKATKATKATKATKATKATKATKATKATKAT 165
QY 214 VTTVDVYKEIFKSS-SPIRTQVPLTNSQCQPHILPHODVLIMCYE 260
Db 166 VTAVVEVKEILKSLVNPDKTVMVLTNSGCLCPPLSANEEYIIMGYE 213

RESULT 14
Q08570 PRELIMINARY; PRT; 261 AA.
AC Q08570;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fritiz (Fragment).
GN BHKFIZ.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97321551; PubMed=9178261;
RA Mayr T., Deutsch U., Kuhl M., Drexler H.C.A., Lottspeich F.,
RA Deutzmann R., Wedlich D., Risau W.;
RT "Fritz: a secreted frizzled-related protein that inhibits Wnt
activity.";
RL Mech. Dev. 63:109-125(1997).
DR EMBL: U91904; AAB51299.1; -.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR001134; Netrin_C.
DR Pfam: PF01392; Fz; 1.
DR Pfam: PF01759; NTR; 1.
DR SMART: SM00063; FRI; 1.
DR PROSITE: PSS0038; Fz; 1.
FT 'NON_TER 261 261
SQ SEQUENCE 261 AA; 29347 MW; BED383DCC70203C1 CRC64;

Query Match 33.1%; Score 621.5; DB 11; Length 261;
Best Local Similarity 47.0%; Pred. No. 6.4e-49;
Matches 131; Conservative 42; Mismatches 73; Indels 33; Gaps 8;

QY 53 NAILAIEQYELVDVNCNAVURFFFCAMYPACTLEFLHDPKCKVCQQRARDCEPLM 112

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DB 2 NXILXIQEGLXTHCXGDLFFLCAMYPACTXDFQREPIKPKCKSVGERARQGCETL 61
QY 113 KMYNHSWPESLACDELPPVYDRGVCISPEAIVTDLPEDVKWIDITPDMVMVQERPLDVC-- 170
DB 62 IKYRHSWPESLACEELPPVYDRGVCISPEAIVTADGADF-----PMSSTGH 107
QY 171 -KRLSPDRCKCKKFTLATYLSKNYVIHAKIKAVORSGCNEVTVVVDVKEIFKSS-S 228
DB 108 XRGASSERCKCKPVTRATXFRNNYNYVIRAKVKEV-KAKCHDVTAVVEKKEILKASLV 166
QY 229 PIPRTOVPLITNSSCOPHLPHQDVLIMCY--EWRSRMMLLENCLVEKWRDOLSKRSIQ 286
DB 167 NIPRDTVNLTYTSGCLCPPLHNEEYIIMGYEDEERSRLLEVETIVEKWKDRXGKXKVR 226
QY 287 WEERLQ-----EQRTVQDKKTKTAGRTSRNPPKPKG 318
DB 227 WDKLRLHGLGKTDASDSTONOK--AGRNSN---PRPAG 260

RESULT 15

Q95JB1 PRELIMINARY; PRT; 130 AA.
AC Q95JB1;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Frizzled protein homolog (Fragment).
GN FRIZ.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KNEE ARTICULAR CARTILAGE;
RA Kataoka H., Enomoto K.;
RT "Partial cDNA sequence isolated by RT-PCR."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB073103; BAB69964.1; -
DR InterPro: IPR000024; F2_domain.
DR Pfam: PF01392; Fz; 1.
DR PROSITE: PS50038; Fz; 1.
FT NON_TER 1
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 14486 MW; 9B39193BF2674721 CRC64;

Query Match 27.2%; Score 512; DB 6; Length 130;
Best Local Similarity 71.2%; Pred. No. 3e-39;
Matches 89; Conservative 15; Mismatches 17; Indels 4; Gaps 1;
QY 29 IPWCRHMPNITRMPNHLHSTOENAILAIEQYEEELVDVNCNAVLRFFFCAMYAPICTLE 88
DB 1 IPLCKSLPWNMTKMPNHLHSTOANAILAIEQFGLGLGTHCSPDLLFFLCAMYAPICTID 60
QY 89 FLHDPIKPKCKVCORARDCEPLMKMNHNSWPESLACDELPPVYDRGVCISPEAIVT---- 144
DB 61 FQHEPIKPKCKSVGERARQGCETLIIKYRHSWPESLACEELPPVYDRGVCISPEAIVTADGA 120
QY 145 DLPEP 149
DB 121 DFPMD 125

Search completed: March 7, 2003, 11:24:59
Job time : 38 secs

infusion vs. oral → evaluation
scope

Variation between maximum.

PP-4

Sept. 2000 bovine

are all maximum. described

W.D. on claim 5.